

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:26:32 : Search time 1840 Seconds
(Without alignments)
807.491 Million cell updates/sec

Title: US-09-626-616-7_COPY_354_424

Perfect score: 71

Sequence: 1 GCACCTGTCGACCCATGC.....ACAGCTGTCCTCGAC 71

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_om.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_hlg_hum.*
31: em_hlg_inv.*
32: em_hlg_other.*
33: em_hlggo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	71	100.0	305	9	HSOPRM11	AF024515 Homo sapi
2	71	100.0	520	11	G53082	G53082 SHGC-84785
3	71	100.0	1203	9	AF286024	AF286024 Macaca mu
4	71	100.0	1399	9	AY038989	AY038989 Macaca fa
5	71	100.0	1610	6	ARI06017	ARI06017 Sequence
6	71	100.0	1610	6	HUMOP10IDA	LI29301 Homo sapien
7	71	100.0	96310	2	AL136444	AL136444 Human DNA
8	71	100.0	182048	9	AC027439	AC027439 Homo sapi
9	71	100.0	182383	2	AC021745	AC021745 Homo sapi
10	69.4	97.7	1182	6	AX280923	AX280923 Sequence
11	69.4	97.7	1203	6	AX280921	AX280921 Sequence
12	69.4	97.7	2160	6	ARI62044	ARI62044 Sequence
13	69.4	97.7	2162	6	A87781	A87781 Sequence
14	69.4	97.7	2162	9	HUMOR1X	LI25119 Human Mu op
15	67.8	95.5	1473	9	HSU12569	LI25569 Human mu op
16	63	88.7	1881	4	PIGMOOPR	LI38645 Sus scrofa
17	61.4	86.5	1415	4	BT089677	BT089677 Bos taurus
18	56.6	79.7	1346	10	AF167566	AF167566 Mus muscu
19	56.6	79.7	1365	10	AF167565	AF167565 Mus muscu
20	56.6	79.7	1367	10	RNI35424	U35424 Rattus norv
21	56.6	79.7	1367	10	RNI35424	U35424 Rattus norv
22	56.6	79.7	1401	10	RATMOP10ID	LI2455 Rat mu opto
23	56.6	79.7	1423	10	AF062753	AF062753 Mus muscu
24	56.6	79.7	1440	10	AF260306	AF260306 Mus muscu
25	56.6	79.7	1440	10	AF400246	AF400246 Mus muscu
26	56.6	79.7	1448	10	RNI02083	U02083 Rattus norv
27	56.6	79.7	1543	10	AF074974	AF074974 Mus muscu
28	56.6	79.7	1569	10	AF260308	AF260308 Mus muscu
29	56.6	79.7	1569	10	AF400248	AF400248 Mus muscu
30	56.6	79.7	1586	10	RATMORA	LI13069 Rattus norv
31	56.6	79.7	1610	10	MMU26915	U26915 Mus musculu
32	56.6	79.7	1614	10	AF260307	AF260307 Mus muscu
33	56.6	79.7	1614	10	AF400247	AF400247 Mus muscu
34	56.6	79.7	1618	6	ARI06013	ARI06013 Sequence
35	56.6	79.7	1618	6	ARI06014	ARI06014 Sequence
36	56.6	79.7	1618	6	ARI53354	ARI53354 Sequence
37	56.6	79.7	1618	6	ARI53355	ARI53355 Sequence
38	56.6	79.7	1729	10	AF167568	AF167568 Mus muscu
39	56.6	79.7	1944	10	S79903	S79903 mu oploid r
40	56.6	79.7	2045	10	AF167567	AF167567 Mus muscu
41	56.6	79.7	2093	10	MMORI	U10558 Mus musculu
42	56.6	79.7	2135	6	ARI48257	ARI48257 Sequence
43	56.6	79.7	2135	10	RATMORA1A	L20684 Rattus norv
44	56.6	79.7	2137	10	AB047546	AB047546 Mus muscu
45	56.6	79.7	2229	6	A68824	A68824 Sequence 1
46	56.6	79.7	2229	10	MMU19380	U19380 Mus musculu
47	56.6	79.7	2397	10	RATROBR	D16349 Rat mRNA fo
48	56.6	79.7	178454	2	AC055776	AC055776 Mus muscu
49	49.2	69.3	6494	6	AX346295	AX346295 Sequence
50	49.2	69.3	6494	6	AX348524	AX348524 Sequence
51	37.4	52.7	6494	6	AX346294	AX346294 Sequence
52	37.4	52.7	6494	6	AX348523	AX348523 Sequence
53	28	39.4	73972	2	AC100554	AC100554 Mus muscu
54	28	39.4	161023	2	AC069508	AC069508 Homo_sapi
55	28	39.4	180223	9	AC062017	AC062017 Homo_sapi
56	27.2	38.3	135666	2	AL513013	AL513013 Homo_sapi
57	26.8	37.7	110551	2	AC103091	AC103091 Rattus no
58	26.8	37.7	119048	2	AP004167	AP004167 Oryza sat
59	26.8	37.7	234777	2	AL670236	AL670236 Mus muscu
60	26.8	37.7	253111	2	AL627204	AL627204 Mus muscu
61	26.8	37.7	254197	2	AF389853	AF389853 Mus muscu
62	26.6	37.5	2051	3	DSU32096	U32096 Drosophila
63	26.6	37.5	10647	1	AE002031	AE002031 Deinococc
64	26.6	37.5	134914	9	AC004542	AC004542 Homo_sapi
65	26.6	37.5	217292	9	AF288742	AF288742 Homo_sapi
66	26.4	37.2	109519	6	AX195929	AX195929 Sequence
67	26.4	37.2	124669	2	AP004325	AP004325 Oryza sat
68	26.4	37.2	159218	2	AL450307	AL450307 Homo_sapi
69	26.2	36.9	785	1	AF338352	AF338352 Cellulomo
70	26.2	36.9	785	9	HSA331011	AJ331011 Homo_sapi
71	26.2	36.9	836	9	HSA342700	AJ342700 Homo_sapi
72	26	36.6	10314	1	AE004600	AE004600 Pseudomon
73	26	36.6	10964	1	AE004892	AE004892 Pseudomon

74	26	36.6	42704	1	SCBAC17A6	AL566248 Streptomy	c 147	25	35.2	193382	2	AC021583	AC021583 Homo sapi
75	26	36.6	70282	2	AP001505	AP001505 Homo sapi	c 148	25	35.2	196612	9	AC021582	AC021582 Homo sapi
76	26	36.6	110000	2	AC091288_1	Continuation (2 of	c 149	25	35.2	212459	9	AC069562	AC069562 Mus muscu
77	26	36.6	110000	2	AC091288_2	Continuation (3 of	c 150	25	35.2	212459	10	AC026385	AC026385 Mus muscu
78	26	36.6	120598	2	OSJ00104	OSJ00104	c 151	25	35.2	225610	10	RME60364	AL60364 Rhizobium
79	26	36.6	158456	9	CNS01DXB	AL139194 Human chr	c 152	24.8	34.9	1072	33	AC050963	AC050963 Giardia 1
80	26	36.6	194523	9	HS323M2	AL028476 Human DNA	c 153	24.8	34.9	2190	6	AX014151	AX014151 Sequence
81	26	36.6	204177	2	AC008761	AC008761 Homo sapi	c 154	24.8	34.9	2281	9	AK025719	AK025719 Homo sapi
82	26	36.6	223169	2	AC091248	AC091248 Homo sapi	c 155	24.8	34.9	4156	9	HSIGF27	X07868 Human DNA f
83	26	36.6	276261	2	HSAC000406	AC000406 Homo sapi	c 156	24.8	34.9	12234	1	AB070953	AB070953 Streptomy
84	26	36.6	340000	9	HS21C101	AL163301 Homo sapi	c 157	24.8	34.9	39210	9	HSE118G4	Z69647 Human DNA s
85	25.8	36.3	12299	1	AE006000	AE006000 Caulobact	c 158	24.8	34.9	50508	9	AC004940	AC004940 Homo sapi
86	25.8	36.3	12497	1	AE004691	AE004691 Pseudomon	c 159	24.8	34.9	78505	2	AC006408	AC006408 Homo sapi
87	25.8	36.3	39741	1	SC8E7	AL331338 Streptomy	c 160	24.8	34.9	100785	9	AP000617	AP000617 Homo sapi
88	25.8	36.3	52173	9	HS66PDGEN	X55448 H.sapiens G	c 161	24.8	34.9	123551	2	AC005809	AC005809 Homo sapi
89	25.8	36.3	121949	2	AP004190	AP004190 Oryza sat	c 162	24.8	34.9	131274	2	AC069506	AC069506 Homo sapi
90	25.8	36.3	159744	2	AP003892	AP003892 Oryza sat	c 163	24.8	34.9	137371	2	AC044908	AC044908 Homo sapi
91	25.8	36.3	219447	9	HUMFLNG6PD	LA4140 Homo sapien	c 164	24.8	34.9	138094	2	AC009417	AC009417 Homo sapi
92	25.8	36.3	346510	1	AP003011	AP003011 Mesorhizo	c 165	24.8	34.9	149628	2	AC034128	AC034128 Homo sapi
93	25.6	36.1	1865	9	HSAl31613	AL131613 Homo sapi	c 166	24.8	34.9	156255	2	AC092903	AC092903 Homo sapi
94	25.6	36.1	1967	9	BC015797	BC015797 Homo sapi	c 167	24.8	34.9	156879	2	AC026957	AC026957 Homo sapi
95	25.6	36.1	1969	9	BC007355	BC007355 Homo sapi	c 168	24.8	34.9	157048	9	AC067744	AC067744 Homo sapi
96	25.6	36.1	2004	6	AX061232	AX061232 Sequence	c 169	24.8	34.9	159129	30	AC023246	AC023246 Homo sapi
97	25.6	36.1	8626	9	HSAl31612	AL131612 Homo sapi	c 170	24.8	34.9	159409	2	AC092900	AC092900 Homo sapi
98	25.6	36.1	18577	9	HSAl	Z93437 Human DNA s	c 171	24.8	34.9	160877	2	AC026560	AC026560 Homo sapi
99	25.6	36.1	125630	2	AC090650	AC090650 Arabidops	c 172	24.8	34.9	163300	2	AC060820	AC060820 Homo sapi
100	25.6	36.1	156028	2	AC025684	AC025684 Homo sapi	c 173	24.8	34.9	165125	2	AC108064	AC108064 Homo sapi
101	25.6	36.1	160839	2	AC069257	AC069257 Homo sapi	c 174	24.8	34.9	165188	9	AP003716	AP003716 Homo sapi
102	25.6	36.1	173068	4	AC091660	AC091660 Bos tauri	c 175	24.8	34.9	166246	2	AF271408	AF271408 Homo sapi
103	25.4	35.8	5551	2	HSAl323418	AL1323418 Homo sapi	c 176	24.8	34.9	171759	2	AC073650	AC073650 Homo sapi
104	25.4	35.8	55501	2	AC107984	AC107984 Homo sapi	c 177	24.8	34.9	183591	9	AC092051	AC092051 Homo sapi
105	25.4	35.8	66933	2	AC101755	AC101755 Mus muscu	c 178	24.8	34.9	191967	2	AC021962	AC021962 Homo sapi
106	25.4	35.8	68066	2	AC110285	AC110285 Homo sapi	c 179	24.8	34.9	200214	2	AL626775	AL626775 Mus muscu
107	25.4	35.8	110000	2	LMFICR31_04	Continuation (5 of	c 180	24.8	34.9	216016	2	AL626775	AL626775 Mus muscu
108	25.4	35.8	117026	9	HS329A5	AC003663 Homo sapi	c 181	24.8	34.9	338579	1	AP003004	AP003004 Mesorhizo
109	25.4	35.8	132070	9	AC003663	AL138781 Human DNA	c 182	24.6	34.6	623	9	HSPRCSH10	U503329 Human prote
110	25.4	35.8	154918	9	AL138781	AC098128 Rattus no	c 183	24.6	34.6	718	9	HSN337288	AL337288 Homo sapi
111	25.4	35.8	175515	2	AC098128	AL590464 Streptomy	c 184	24.6	34.6	14439	1	AE004655	AE004655 Pseudomon
112	25.4	35.8	178073	1	SC0590464	AC027601 Homo sapi	c 185	24.6	34.6	23786	9	HS415C1	Z98472 Human DNA s
113	25.4	35.8	191222	2	AC07461	AC07461 Homo sapi	c 186	24.6	34.6	24790	1	AB070946	AB070946 Streptomy
114	25.4	35.8	201602	2	AC074146	AC074146 Mus muscu	c 187	24.6	34.6	35350	9	AF414442	AF414442 Homo sapi
115	25.4	35.8	204940	2	AC069007	AC069007 Homo sapi	c 188	24.6	34.6	39170	2	AC005202	AC005202 Homo sapi
116	25.4	35.8	204969	2	AC091132	AC091132 Homo sapi	c 189	24.6	34.6	40356	1	SC16	AL59519 Streptomy
117	25.4	35.8	229482	2	AC074149	AC074149 Mus muscu	c 190	24.6	34.6	51920	2	CER08A5	Z82881 Caenorhabdi
118	25.2	35.5	864	5	SCR20	AB072353 Aldabrach	c 191	24.6	34.6	86767	2	AL106263	AL106263 Rattus no
119	25.2	35.5	17856	1	SCR20	AL504057 Streptomy	c 192	24.6	34.6	92509	1	AL646086	AL646086 Ralstonia
120	25.2	35.5	22134	1	SC152	AL504057 Streptomy	c 193	24.6	34.6	95280	9	AC073133	AC073133 Homo sapi
121	25.2	35.5	34725	1	SC1B2	AL356812 Streptomy	c 194	24.6	34.6	98771	2	AC025044	AC025044 Oryza sat
122	25.2	35.5	44160	9	AC0000049	AC0000049 Homo sapi	c 195	24.6	34.6	111977	2	AP000717	AP000717 Homo sapi
123	25.2	35.5	60432	2	AC102080	AC102080 Mus muscu	c 196	24.6	34.6	123469	2	AC097087	AC097087 Rattus no
124	25.2	35.5	66400	2	AC1015064	AC1015064 Drosophill	c 197	24.6	34.6	133069	2	AC026836	AC026836 Homo sapi
125	25.2	35.5	118914	5	AC094011	AC094011 Gallus ga	c 198	24.6	34.6	133655	9	AL357274	AL357274 Human DNA
126	25.2	35.5	135509	8	AC037426	AC037426 Oryza sat	c 199	24.6	34.6	152397	8	AC027660	AC027660 Oryza sat
127	25.2	35.5	139726	2	AC096306	AC096306 Rattus no	c 200	24.6	34.6	157122	2	AC105491	AC105491 Rattus no
128	25.2	35.5	157533	9	AL354709	AL354709 Human DNA	c 201	24.6	34.6	157564	2	AC025996	AC025996 Homo sapi
129	25.2	35.5	163052	3	AC007472	AC007472 Drosophill	c 202	24.6	34.6	157762	9	AP001893	AP001893 Homo sapi
130	25.2	35.5	171491	2	AC022606	AC022606 Homo sapi	c 203	24.6	34.6	161610	2	AC011728	AC011728 Homo sapi
131	25.2	35.5	189370	1	AF010496	AF010496 Rhodobact	c 204	24.6	34.6	168995	2	AP002359	AP002359 Homo sapi
132	25.2	35.5	221372	2	AL390778	AL390778 Homo sapi	c 205	24.6	34.6	171179	2	AC034140	AC034140 Homo sapi
133	25.2	35.5	265387	3	AE003820	AE003820 Drosophill	c 206	24.6	34.6	180238	2	AC073688	AC073688 Mus muscu
134	25.2	35.5	349498	1	AP003002	AP003002 Mesorhizo	c 207	24.6	34.6	185324	2	AC026265	AC026265 Homo sapi
135	25	35.2	2042	3	DSU32097	U32097 Drosophilla	c 208	24.6	34.6	197126	2	AC023130	AC023130 Homo sapi
136	25	35.2	2056	3	DSU32095	U32095 Drosophilla	c 209	24.6	34.6	200920	2	AC069319	AC069319 Homo sapi
137	25	35.2	2057	3	DSU32094	U32094 Drosophilla	c 210	24.6	34.6	201380	2	AC092905	AC092905 Homo sapi
138	25	35.2	2069	3	DMU32091	U32091 Drosophilla	c 211	24.6	34.6	205317	9	AC093856	AC093856 Homo sapi
139	25	35.2	3759	9	AF153500	AF153500 Homo sapi	c 212	24.6	34.6	210827	2	AL626806	AL626806 Mus muscu
140	25	35.2	5931	1	SC1A6	AL499607 Streptomy	c 213	24.6	34.6	260418	2	AE006463	AE006463 Homo sapi
141	25	35.2	34962	1	SCG20A	AL360055 Streptomy	c 214	24.6	34.6	260967	2	AC091771	AC091771 Homo sapi
142	25	35.2	43147	1	SC4A10	AL109653 Streptomy	c 215	24.4	34.4	3527	1	SHU51222	U51222 Streptomyce
143	25	35.2	143291	9	HS163G9	AL1008733 Human DNA	c 216	24.4	34.4	4171	1	MLUDN1A2	M34006 M.luteus ri
144	25	35.2	159702	9	AL356433	AL356433 Human DNA	c 217	24.4	34.4	14980	1	SC4A9	AL138668 Streptomy
145	25	35.2	166206	2	AC016927	AC016927 Homo sapi	c 218	24.4	34.4	71793	2	AC101733	AC101733 Mus muscu
146	25	35.2	172460	2	AC079798	AC079798 Homo sapi	c 219	24.4	34.4	78184	9	AC067722	AC067722 Homo sapi

C 220	24.4	34.4	79414	2	AC023502	Homo sapi	293	24	33.8	3274	1	AB020341
C 221	24.4	34.4	104228	2	AL354751	Human DNA	294	24	33.8	3387	6	AX235185
C 222	24.4	34.4	110000	2	AC107387_2	Continuation (3 of	295	24	33.8	3810	6	AK000048
C 223	24.4	34.4	122436	10	AB051897	Mus muscu	296	24	33.8	3900	6	AX235183
C 224	24.4	34.4	148348	2	AC104074	Homo sapi	C 297	24	33.8	7291	1	AE009865
C 225	24.4	34.4	154732	2	AC023236	Homo sapi	C 298	24	33.8	11103	1	AE004774
C 226	24.4	34.4	160682	2	AC099675	Homo sapi	C 299	24	33.8	12152	6	AX196110
C 227	24.4	34.4	164073	2	AC008032	Homo sapi	C 300	24	33.8	13345	1	AE004640
C 228	24.4	34.4	166181	9	HS37E16	Human DNA	C 301	24	33.8	18751	1	AF121000
C 229	24.4	34.4	174992	2	AC025622	Homo sapi	C 302	24	33.8	18106	1	DNAVRL01
C 230	24.4	34.4	176543	2	AC025871	Homo sapi	C 303	24	33.8	32360	1	AC005339
C 231	24.4	34.4	178324	2	AC018828	Homo sapi	C 304	24	33.8	35101	1	SC6E78
C 232	24.4	34.4	180629	2	AC104075	Homo sapi	C 305	24	33.8	36224	1	SCD78
C 233	24.4	34.4	181210	2	AC011742	Homo sapi	C 306	24	33.8	42010	10	AC002298
C 234	24.4	34.4	188631	9	AC022383	Homo sapi	C 307	24	33.8	43872	9	AL358782
C 235	24.4	34.4	194070	2	AL663075	Mus muscu	C 308	24	33.8	47730	10	MMWHNGENE
C 236	24.4	34.4	200050	1	AL646068	Rattus no	C 309	24	33.8	75609	9	AL162416
C 237	24.4	34.4	202793	9	CNS06C83	Human chr	C 310	24	33.8	86896	1	RCU57682
C 238	24.4	34.4	210047	9	AC022384	AL391158	C 311	24	33.8	93172	2	AL357872
C 239	24.4	34.4	212855	2	AL596122	Mus muscu	C 312	24	33.8	93650	2	AL359635_4
C 240	24.4	34.4	216184	2	AC055773	Mus muscu	C 313	24	33.8	108930	2	AL513122
C 241	24.4	34.4	216381	2	AC011132	Homo sapi	C 314	24	33.8	110000	2	AL359635_3
C 242	24.4	34.4	217346	9	AC012363	Homo sapi	C 315	24	33.8	111977	2	AP000717
C 243	24.4	34.4	226758	9	AC006449	Homo sapi	C 316	24	33.8	115936	2	AL445205
C 244	24.4	34.4	322593	2	AC107084	Homo sapi	C 317	24	33.8	118183	2	AC090433
C 245	24.4	34.4	349116	1	AP003003	Mesorhizo	C 318	24	33.8	118313	9	AC003991
C 246	24.2	34.1	609	11	AU047620	Rattus no	C 319	24	33.8	130000	9	AC087259
C 247	24.2	34.1	677	8	AF261173	Saxifraga	C 320	24	33.8	139097	2	AC004591
C 248	24.2	34.1	1440	6	AF147705	Rhodobact	C 321	24	33.8	141469	9	AL139811
C 249	24.2	34.1	1782	6	AX103432	Sequence	C 322	24	33.8	143285	9	AL139423
C 250	24.2	34.1	1799	9	BC003533	Homo sapi	C 323	24	33.8	145063	2	AC027069
C 251	24.2	34.1	1804	6	AX355684	Sequence	C 324	24	33.8	151075	2	AC022594
C 252	24.2	34.1	1877	9	AK027669	Homo sapi	C 325	24	33.8	152129	2	AC027416
C 253	24.2	34.1	1944	6	AX103428	Sequence	C 326	24	33.8	155818	9	AC073504
C 254	24.2	34.1	2439	6	BC009383	Homo sapi	C 327	24	33.8	155885	9	AL442646
C 255	24.2	34.1	2439	6	AX059564	Sequence	C 328	24	33.8	155606	2	AC068038
C 256	24.2	34.1	2815	1	SLOCURS	X58793 S. lividans	C 329	24	33.8	157001	2	CNS07EP5
C 257	24.2	34.1	3167	1	AF019038	Pseudomon	C 330	24	33.8	157762	9	AP001893
C 258	24.2	34.1	5066	10	MMU132389	Mus muscu	C 331	24	33.8	158297	9	AC106779
C 259	24.2	34.1	8934	10	MUSBR2R	L27595 Mus muscarti	C 332	24	33.8	158995	2	AL590679
C 260	24.2	34.1	10602	1	AE004874	Pseudomon	C 333	24	33.8	159748	2	AC016712
C 261	24.2	34.1	20850	1	SC2E9	AL021530 Streptomy	C 334	24	33.8	161610	2	AC011728
C 262	24.2	34.1	33311	9	AC004235	Homo sapi	C 335	24	33.8	162328	9	AP000350
C 263	24.2	34.1	43804	6	A93469	Sequence 1	C 336	24	33.8	163144	2	AL365399
C 264	24.2	34.1	43804	6	A98892	Sequence 1	C 337	24	33.8	165960	2	AL162452
C 265	24.2	34.1	43804	14	AU046933	U46933 Avian adeno	C 338	24	33.8	168995	2	AP002359
C 266	24.2	34.1	52664	2	AC097284	Rattus no	C 339	24	33.8	169296	2	AC022198
C 267	24.2	34.1	57205	2	AC107995	Homo sapi	C 340	24	33.8	170114	2	AC016143
C 268	24.2	34.1	66948	2	AC100203	Mus muscu	C 341	24	33.8	171985	9	AL445675
C 269	24.2	34.1	147000	9	AP004242	Homo sapi	C 342	24	33.8	173025	9	CNS07TIV
C 270	24.2	34.1	152862	2	OSJN00168	Sequence	C 343	24	33.8	174764	9	AC108879
C 271	24.2	34.1	180341	2	AC099468	Rattus no	C 344	24	33.8	175562	2	AL139242
C 272	24.2	34.1	181339	9	AC027591	Homo sapi	C 345	24	33.8	176578	2	AC041008
C 273	24.2	34.1	183249	2	AC004828	Homo sapi	C 346	24	33.8	177156	2	AC106469
C 274	24.2	34.1	189344	2	AL627235	Mus muscu	C 347	24	33.8	177632	2	AC024098
C 275	24.2	34.1	192864	2	AC040981	Mus muscu	C 348	24	33.8	181029	30	AC026901
C 276	24.2	34.1	194296	9	AL354864	Human DNA	C 349	24	33.8	181175	9	AL186214
C 277	24.2	34.1	194622	2	AL645976	Mus muscu	C 350	24	33.8	182044	2	AL355872
C 278	24.2	34.1	199306	2	AC068459	Homo sapi	C 351	24	33.8	182048	2	AC091399
C 279	24.2	34.1	207184	2	AC020664	Homo sapi	C 352	24	33.8	183247	2	AL359749
C 280	24.2	34.1	303717	2	AC063930	Homo sapi	C 353	24	33.8	184222	2	AL356292
C 281	24.2	34.1	341887	1	AP003006	Mesorhizo	C 354	24	33.8	185324	2	AC026265
C 282	24.2	34.1	348077	1	AP003000	Mesorhizo	C 355	24	33.8	189324	2	AC097532
C 283	24.2	33.8	852	6	AX196125	Sequence	C 356	24	33.8	190595	9	AC009522
C 284	24.2	33.8	1113	9	AF090833	Streptomy	C 357	24	33.8	192550	2	AC025584
C 285	24.2	33.8	1415	1	HSGE13	Human gene	C 358	24	33.8	193168	2	AC011969
C 286	24.2	33.8	1524	6	AX106328	Sequence	C 359	24	33.8	193814	2	AL512326
C 287	24.2	33.8	1524	6	AX140619	Sequence	C 360	24	33.8	197019	9	AL157938
C 288	24.2	33.8	1524	6	AX200479	Sequence	C 361	24	33.8	198490	2	AC022983
C 289	24.2	33.8	1524	6	AX267135	Sequence	C 362	24	33.8	205414	2	AC027309
C 290	24.2	33.8	1548	6	AX018184	Sequence	C 363	24	33.8	208975	2	AC012465
C 291	24.2	33.8	2981	9	AK000235	Homo sapi	C 364	24	33.8	217238	2	AL591131
C 292	24.2	33.8	3115	1	DG1318781	Desulfiovi	C 365	24	33.8	227482	2	AC008735
C 293	24.2	33.8	3274	1	AB020341	Desulfiovi	C 366	24	33.8	227482	2	AC008735
C 294	24.2	33.8	3387	6	AX235185	Sequence	C 367	24	33.8	227482	2	AC008735
C 295	24.2	33.8	3810	6	AK000048	Homo sapi	C 368	24	33.8	227482	2	AC008735
C 296	24.2	33.8	3900	6	AX235183	Sequence	C 369	24	33.8	227482	2	AC008735
C 297	24.2	33.8	7291	1	AE009865	Alcaligenes	C 370	24	33.8	227482	2	AC008735
C 298	24.2	33.8	11103	1	AE004774	Pseudomon	C 371	24	33.8	227482	2	AC008735
C 299	24.2	33.8	12152	6	AX196110	Sequence	C 372	24	33.8	227482	2	AC008735
C 300	24.2	33.8	13345	1	AE004640	Pseudomon	C 373	24	33.8	227482	2	AC008735
C 301	24.2	33.8	18751	1	AF121000	Corynebac	C 374	24	33.8	227482	2	AC008735
C 302	24.2	33.8	18106	1	DNAVRL01	U20246 Dichelobact	C 375	24	33.8	227482	2	AC008735
C 303	24.2	33.8	32360	1	AC005339	Homo sapi	C 376	24	33.8	227482	2	AC008735
C 304	24.2	33.8	35101	1	SC6E78	AL079348 Streptomy	C 377	24	33.8	227482	2	AC008735
C 305	24.2	33.8	36224	1	SCD78	AL034355 Streptomy	C 378	24	33.8	227482	2	AC008735
C 306	24.2	33.8	42010	10	AC002298	Genomic S	C 379	24	33.8	227482	2	AC008735
C 307	24.2	33.8	43872	9	AL358782	Human DNA	C 380	24	33.8	227482	2	AC008735
C 308	24.2	33.8	47730	10	MMWHNGENE	Y12488 M. musculus	C 381	24	33.8	227482	2	AC008735
C 309	24.2	33.8	75609	9	AL162416	U57682 Rhodobacter	C 382	24	33.8	227482	2	AC008735
C 310	24.2	33.8	86896	1	RCU57682	AL357872 Human DNA	C 383	24	33.8	227482	2	AC008735
C 311	24.2	33.8	93172	2	AL359635_4	Continuation (5 of	C 384	24	33.8	227482	2	AC008735
C 312	24.2	33.8	93650	2	AL359635_4	Continuation (4 of	C 385	24	33.8	227482	2	AC008735
C 313	24.2	33.8	108930	2	AL513122	Continuation (4 of	C 386	24	33.8	227482	2	AC008735
C 314	24.2	33.8	110000	2	AL359635_3	Continuation (4 of	C 387	24	33.8	227482	2	AC008735
C 315	24.2	33.8	111977	2	AP000717	Homo sapi	C 388	24	33.8	227482	2	AC008735
C 316	24.2	33.8	115936	2	AL445205	Human DNA	C 389	24	33.8	227482	2	AC008735
C 317	24.2	33.8	118183	2	AC090433	Chlamydom	C 390	24	33.8	227482	2	AC008735
C 318	24.2	33.8	118313	9	AC003991	Human BAC	C 391	24	33.8	227482	2	AC008735
C 319	24.2	33.8	130000	9	AC087259	Homo sapi	C 392	24	33.8	227482	2	AC008735
C 320	24.2	33.8	139097	2	AC004591	Mus muscu	C 393	24	33.8	227482	2	AC008735
C 321</												

C 366	24	33.8	234381	2	AC074152	AC074152 Mus muscu	C 439	23.6	33.2	1110	4	SSFGDMR	X16638 Pig pgd mRNA
C 367	24	33.8	326249	2	AC034210	AC034210 Homo sapi	C 440	23.6	33.2	1124	11	G07120	G07120 human STS w
C 368	24	33.8	347660	1	AP002994	AP002994 Mesorhizo	C 441	23.6	33.2	1439	9	S71481S1	S71481S1 granuloocyte
C 369	24	33.8	347750	1	AP002998	AP002998 Mesorhizo	C 442	23.6	33.2	1540	1	REU83846	REU83846 Rhodococcus
C 370	23.8	33.5	553	1	MBMPB57	X13970 Mycobacteri	C 443	23.6	33.2	1651	9	HUMIGR1PR	HUMIGR1PR Human insul
C 371	23.8	33.5	553	1	MBMPB57A	M35389 M.bovis Imm	C 444	23.6	33.2	1714	8	AIERG3	AIERG3 Human insul
C 372	23.8	33.5	553	6	E02260	E02260 DNA sequenc	C 445	23.6	33.2	1786	9	H0M1LGFIR	H0M1LGFIR Human insul
C 373	23.8	33.5	583	6	RABIGHXO	M93185 Oryctolagus	C 446	23.6	33.2	1869	9	H83519	H83519 Human insul
C 374	23.8	33.5	597	6	AX073942	AX073942 Sequence	C 447	23.6	33.2	2156	6	I58541	I58541 Sequence 1
C 375	23.8	33.5	671	1	MSG10KAG	M25258 Mycobacteri	C 448	23.6	33.2	2156	9	HUMRANES	HUMRANES Human sapien
C 376	23.8	33.5	914	1	MTBCGA	X13739 Mycobacteri	C 449	23.6	33.2	2214	9	HUMH145	HUMH145 Human insul
C 377	23.8	33.5	1005	5	FUNLACDK	L23793 Fundulus he	C 450	23.6	33.2	4086	9	GA4291729	GA4291729 Gallus ga
C 378	23.8	33.5	1965	5	AK024529	AK024529 Homo sapi	C 451	23.6	33.2	4993	1	TA4HCCOR	TA4HCCOR Thauera a
C 379	23.8	33.5	2181	6	AR103051	AR103051 Sequence	C 452	23.6	33.2	11639	1	SCBAC8D1	SCBAC8D1 Streptomy
C 380	23.8	33.5	2376	6	AX001334	AX001334 Sequence	C 453	23.6	33.2	16405	1	AB041030	AB041030 Arthrobac
C 381	23.8	33.5	2376	10	MMSOX1	X94126 M. musculus	C 454	23.6	33.2	25342	1	AL157892	AL157892 Human DNA
C 382	23.8	33.5	2987	1	MTGROBP	X60532 M. tuberculosis	C 455	23.6	33.2	36368	1	SC9B5	SC9B5 Streptomy
C 383	23.8	33.5	3025	5	CHKFRZAL	D10875 Gallus gall	C 456	23.6	33.2	49736	1	AF319998	AF319998 Stigmatel
C 384	23.8	33.5	3175	1	RM019726	U19726 Rhizobium m	C 457	23.6	33.2	67945	2	AC104887	AC104887 Mus muscu
C 385	23.8	33.5	4300	1	BP012276	U12276 Bordetella	C 458	23.6	33.2	69104	2	AC096014	AC096014 Rattus no
C 386	23.8	33.5	9004	1	SM059239	U59239 Serratia ma	C 459	23.6	33.2	69683	2	AC106115	AC106115 Rattus no
C 387	23.8	33.5	10029	1	AE005310	AE005310 Escherich	C 460	23.6	33.2	72857	2	AC094297	AC094297 Rattus no
C 388	23.8	33.5	10401	1	AE004584	AE004584 Pseudomon	C 461	23.6	33.2	90780	2	AC020777	AC020777 Homo sapi
C 389	23.8	33.5	11519	1	AE004616	AE004616 Pseudomon	C 462	23.6	33.2	90325	9	AL591803	AL591803 Human DNA
C 390	23.8	33.5	12075	1	AE004641	AE004641 Pseudomon	C 463	23.6	33.2	96892	8	ATF14E8	ATF14E8 Arabidops
C 391	23.8	33.5	12130	1	AE005133	AE005133 Halobacte	C 464	23.6	33.2	110467	8	AF381614	AF381614 Magnapor
C 392	23.8	33.5	12820	1	AE005273	AE005273 Escherich	C 465	23.6	33.2	114929	9	AC002401	AC002401 Homo sapi
C 393	23.8	33.5	13922	1	AE001894	AE001894 Deinococce	C 466	23.6	33.2	134594	2	AL358433	AL358433 Homo sapi
C 394	23.8	33.5	15372	1	AE007158	AE007158 Mycobacte	C 467	23.6	33.2	138168	2	AL445245	AL445245 Homo sapi
C 395	23.8	33.5	29698	4	SSRYRA	X69465 S. scrofa ge	C 468	23.6	33.2	139512	2	HSJ1169J3	HSJ1169J3 Human DNA
C 396	23.8	33.5	33818	1	MTCT78	Z77185 Mycobacteri	C 469	23.6	33.2	150594	2	AP000728	AP000728 Homo sapi
C 397	23.8	33.5	36277	9	AP000336	AP000336 Homo sapi	C 470	23.6	33.2	158052	9	AC027612	AC027612 Homo sapi
C 398	23.8	33.5	35583	1	SC5H1	AL049863 Streptomy	C 471	23.6	33.2	164059	2	AC106135	AC106135 Rattus no
C 399	23.8	33.5	55838	2	AC078792	AL078792 Homo sapi	C 472	23.6	33.2	164144	2	AC101257	AC101257 Homo sapi
C 400	23.8	33.5	58328	2	AC013967	AC013967 Drosophill	C 473	23.6	33.2	164715	2	AC096683	AC096683 Gallus ga
C 401	23.8	33.5	69221	2	AC103480	AC103480 Rattus no	C 474	23.6	33.2	165079	2	AC024517	AC024517 Homo sapi
C 402	23.8	33.5	84491	2	AL645728	AL645728 Homo sapi	C 475	23.6	33.2	166218	2	AC009293	AC009293 Homo sapi
C 403	23.8	33.5	89222	8	NCB1F11	AL670011 Neurospor	C 476	23.6	33.2	168558	2	AC006948	AC006948 Homo sapi
C 404	23.8	33.5	90763	8	NCB10H4	AL670012 Neurospor	C 477	23.6	33.2	171222	2	AC011825	AC011825 Homo sapi
C 405	23.8	33.5	100000	9	AP000215	AP000215 Homo sapi	C 478	23.6	33.2	175529	2	AL591916	AL591916 Homo sapi
C 406	23.8	33.5	104480	2	AC007905	AC007905 Homo sapi	C 479	23.6	33.2	179554	2	AC073268	AC073268 Homo sapi
C 407	23.8	33.5	109329	2	AL157945	AL157945 Homo sapi	C 480	23.6	33.2	182428	2	AC036167	AC036167 Homo sapi
C 408	23.8	33.5	109431	9	AC016696	AC016696 Homo sapi	C 481	23.6	33.2	182724	2	AC025279	AC025279 Homo sapi
C 409	23.8	33.5	152936	9	AC013719	AC013719 Homo sapi	C 482	23.6	33.2	183382	2	AL157388	AL157388 Human DNA
C 410	23.8	33.5	160420	2	AC097626	AC097626 Homo sapi	C 483	23.6	33.2	183920	2	AC023814	AC023814 Homo sapi
C 411	23.8	33.5	161117	3	AC008311	AC008311 Drosophill	C 484	23.6	33.2	184511	2	AC011721	AC011721 Homo sapi
C 412	23.8	33.5	164270	14	AB049735	AB049735 Gallid he	C 485	23.6	33.2	187540	2	AC073970	AC073970 Homo sapi
C 413	23.8	33.5	164270	14	AB049735	AB049735 Gallid he	C 486	23.6	33.2	188928	2	AC020612	AC020612 Homo sapi
C 414	23.8	33.5	170962	2	AL389927	AL389927 Homo sapi	C 487	23.6	33.2	189116	9	CNS01DMM	CNS01DMM Human chr
C 415	23.8	33.5	172748	2	AC097417	AC097417 Rattus no	C 488	23.6	33.2	189142	2	AC074038	AC074038 Homo sapi
C 416	23.8	33.5	173785	9	AP000355	AP000355 Homo sapi	C 489	23.6	33.2	192519	10	MM0278435	MM0278435 Mus muscu
C 417	23.8	33.5	175594	9	AL162503	AL162503 Human DNA	C 490	23.6	33.2	193101	2	AC009561	AC009561 Homo sapi
C 418	23.8	33.5	176756	2	AC099152	AC099152 Rattus no	C 491	23.6	33.2	195028	30	AC024739	AC024739 Homo sapi
C 419	23.8	33.5	177632	2	AC093615	AC093615 Homo sapi	C 492	23.6	33.2	197331	2	AC104439	AC104439 Homo sapi
C 420	23.8	33.5	177632	2	AC093615	AC093615 Homo sapi	C 493	23.6	33.2	199075	2	AC079218	AC079218 Mus muscu
C 421	23.8	33.5	180941	2	AC019219	AC019219 Homo sapi	C 494	23.6	33.2	200137	2	AC104662	AC104662 Homo sapi
C 422	23.8	33.5	182760	2	AC0094052	AC0094052 Rattus no	C 495	23.6	33.2	203108	2	CNS05TC3	CNS05TC3 Human chr
C 423	23.8	33.5	184476	2	AC009113	AC009113 Homo sapi	C 496	23.6	33.2	207389	2	AC009634	AC009634 Homo sapi
C 424	23.8	33.5	197225	2	AC093835	AC093835 Homo sapi	C 497	23.6	33.2	215650	2	AC090469	AC090469 Homo sapi
C 425	23.8	33.5	197360	2	AC018829	AC018829 Homo sapi	C 498	23.6	33.2	216554	2	AC005563	AC005563 Homo sapi
C 426	23.8	33.5	197748	2	AC026283	AC026283 Homo sapi	C 499	23.6	33.2	220965	2	HSA312688	HSA312688 Homo sapi
C 427	23.8	33.5	199938	9	AL162591	AL162591 Human DNA	C 500	23.6	33.2	223335	2	AL392187	AL392187 Homo sapi
C 428	23.8	33.5	202050	1	AL164065	AL164065 Ralstonia	C 501	23.6	33.2	223956	2	AC096324	AC096324 Rattus no
C 429	23.8	33.5	211309	2	AC011896	AC011896 Homo sapi	C 502	23.6	33.0	440	8	HS90D2R	HS90D2R H.sapiens C
C 430	23.8	33.5	217442	2	AC073747	AC073747 Mus muscu	C 503	23.6	33.0	440	8	AF107133	AF107133 Picea ab
C 431	23.8	33.5	230372	2	AC073693	AC073693 Mus muscu	C 504	23.6	33.0	617	9	HSA339116	HSA339116 Homo sapi
C 432	23.8	33.5	236195	2	AC073713	AC073713 Mus muscu	C 505	23.6	33.0	647	9	HSA338944	HSA338944 Homo sapi
C 433	23.8	33.5	286550	1	SME591785	AL591785 Slinorhizo	C 506	23.6	33.0	1002	9	BC002648	BC002648 Homo sapi
C 434	23.8	33.5	303626	1	AE003601	AE003601 Drosophill	C 507	23.6	33.0	2071	3	DM032087	DM032087 Drosophilla
C 435	23.8	33.5	327773	1	AP002554	AP002554 Escherich	C 508	23.6	33.0	2071	3	DM032088	DM032088 Drosophilla
C 436	23.8	33.5	340000	1	AP001760	AP001760 Homo sapi	C 509	23.6	33.0	2071	3	DM032089	DM032089 Drosophilla
C 437	23.6	33.2	390	6	AX069537	AX069537 Sequence	C 510	23.4	33.0	2072	3	DM032090	DM032090 Drosophilla
C 438	23.6	33.2	750	9	HSA330206	HSA330206 Homo sapi	C 511	23.4	33.0	3009	3	AY070882	AY070882 Drosophill

512	23.4	33.0	3433	3	AY060442	Drosophill	C 585	23.2	32.7	1077	33	AC045954	AC045954 Giardia i
513	23.4	33.0	3992	3	AF033117	Drosophill	C 586	23.2	32.7	1187	1	BACESTERAS	124749 Bacillus su
514	23.4	33.0	4119	9	AB040936	Homo sapi	C 587	23.2	32.7	1267	9	BC001809	BC001809 Homo sapi
C 515	23.4	33.0	4120	1	SC6D7A		588	23.2	32.7	1267	9	BC001824	BC001824 Homo sapi
C 516	23.4	33.0	4517	1	CCRPENP1E		C 589	23.2	32.7	1491	9	AB018401	AB018401 Homo sapi
517	23.4	33.0	6290	9	HSMB01391	Homo sapi	C 590	23.2	32.7	1525	1	AF056081	AF056081 Bacillus
C 518	23.4	33.0	10636	1	AE005917	Caulobact	C 591	23.2	32.7	1838	6	E59850	E59850 Method for
C 519	23.4	33.0	10831	1	AE002069	Caulobact	C 592	23.2	32.7	1838	6	E65171	E65171 Method for
520	23.4	33.0	13101	1	AE005948	Caulobact	C 593	23.2	32.7	1954	9	AF141972	AF141972 Pongo pyg
C 521	23.4	33.0	18471	1	SCBAC17E8		C 594	23.2	32.7	2351	1	AF185273	AF185273 Burkholde
522	23.4	33.0	22775	1	SC5G8		C 595	23.2	32.7	2480	8	AF068635	AF068635 Chlamydom
C 523	23.4	33.0	31896	2	AC017879	Streptomy	C 596	23.2	32.7	3157	2	AC019519	AC019519 Drosophill
524	23.4	33.0	33154	1	AF361470	Rhizobium	C 597	23.2	32.7	3276	1	PAPBPC	X55517 P.aeruginos
C 525	23.4	33.0	39619	2	AC017644	Drosophill	C 598	23.2	32.7	3276	3	AF145637	AF145637 Drosophill
526	23.4	33.0	48975	2	AC008998	Homo sapi	C 599	23.2	32.7	3949	9	AF043897	AF043897 Homo sapi
C 527	23.4	33.0	50714	2	AC005471	Drosophill	C 600	23.2	32.7	4294	8	AF362957	AF362957 Aspergill
C 528	23.4	33.0	65088	2	AC084720	Homo sapi	C 601	23.2	32.7	4605	9	HUMPERP	D43639 Human gene
529	23.4	33.0	86824	2	AC015884	Homo sapi	C 602	23.2	32.7	4606	9	S73906	S73906 adrenomedul
C 530	23.4	33.0	96135	2	AC091070	Homo sapi	C 603	23.2	32.7	5400	9	AF211847	AF211847 Homo sapi
531	23.4	33.0	99395	2	AC010446	Homo sapi	C 604	23.2	32.7	6405	9	AB032946	AB032946 Homo sapi
C 532	23.4	33.0	108661	9	AC034214	Homo sapi	C 605	23.2	32.7	6816	6	AR175747	AR175747 Sequence
C 533	23.4	33.0	110098	9	ALJ358976	Human DNA	C 606	23.2	32.7	6835	6	AR175748	AR175748 Sequence
C 534	23.4	33.0	116561	9	HS753P9	Human DNA	C 607	23.2	32.7	6990	9	AF142567	AF142567 Homo sapi
C 535	23.4	33.0	121474	2	AC007150	Drosophill	C 608	23.2	32.7	8366	1	AF072709	AF072709 Streptomy
536	23.4	33.0	122645	2	AC058812	Homo sapi	C 609	23.2	32.7	9449	14	D84262	D84262 Hepatitis C
C 537	23.4	33.0	123039	2	AC093087	Homo sapi	C 610	23.2	32.7	9984	1	ASP290449	ASP290449 Amycolato
538	23.4	33.0	133155	2	AC011910	Drosophill	C 611	23.2	32.7	10126	1	AE004653	AE004653 Pseudomon
C 539	23.4	33.0	133765	9	HS67E13	Human DNA	C 612	23.2	32.7	11445	1	AE004490	AE004490 Pseudomon
C 540	23.4	33.0	143299	9	ALJ353619	Human DNA	C 613	23.2	32.7	12965	1	AE002048	AE002048 Deinococc
C 541	23.4	33.0	145068	9	HSDJ377B1	Human DNA	C 614	23.2	32.7	14015	1	AE0050776	AE0050776 Caulobact
C 542	23.4	33.0	150681	2	AC006011	Homo sapi	C 615	23.2	32.7	17228	1	SC3FE0	SC3FE0 Streptomy
C 543	23.4	33.0	152118	2	AC013263	Homo sapi	C 616	23.2	32.7	18479	1	SC3FE0	SC3FE0 Streptomy
C 544	23.4	33.0	152974	2	AC0106213	Rattus no	C 617	23.2	32.7	19304	1	AB045311	AB045311 Xanthomon
545	23.4	33.0	154788	2	AC031984	Homo sapi	C 618	23.2	32.7	23764	3	AC006723	AC006723 Caenorhab
C 546	23.4	33.0	157134	2	AC106642	Rattus no	C 619	23.2	32.7	25595	1	AF228583	AF228583 Burkholde
C 547	23.4	33.0	159021	2	AC087388	Homo sapi	C 620	23.2	32.7	27854	9	AL450463	AL450463 Human DNA
548	23.4	33.0	160301	3	AC007413	Drosophill	C 621	23.2	32.7	28712	9	CNS00YVC	AL0550463 Human DNA
549	23.4	33.0	160457	2	AC008049	Homo sapi	C 622	23.2	32.7	29466	9	AF252549	AF252549 Homo sapi
550	23.4	33.0	163162	2	AC006247	Drosophill	C 623	23.2	32.7	29516	3	AC010840	AC010840 Drosophill
C 551	23.4	33.0	167679	9	AC007570	Homo sapi	C 624	23.2	32.7	36839	2	AC006181	AC006181 Homo sapi
C 552	23.4	33.0	168009	9	AC090954	Homo sapi	C 625	23.2	32.7	48217	9	AC073932	AC073932 Homo sapi
C 553	23.4	33.0	170758	9	AC004965	Homo sapi	C 626	23.2	32.7	53870	3	AE003163	AE003163 Drosophill
554	23.4	33.0	172904	3	AC007414	Drosophill	C 627	23.2	32.7	66846	2	AC105000	AC105000 Homo sapi
C 555	23.4	33.0	177503	9	AC005297	Homo sapi	C 628	23.2	32.7	69348	2	AC105107	AC105107 Homo sapi
C 556	23.4	33.0	179009	9	AC079802	Homo sapi	C 629	23.2	32.7	74436	2	AC026625	AC026625 Homo sapi
C 557	23.4	33.0	181321	9	AC093179	Homo sapi	C 630	23.2	32.7	77191	2	AC023381	AC023381 Homo sapi
558	23.4	33.0	182039	3	AC099026	Drosophill	C 631	23.2	32.7	77191	2	AC023381	AC023381 Homo sapi
C 559	23.4	33.0	187928	2	AC093624	Homo sapi	C 632	23.2	32.7	78025	9	HS780M13	HS780M13 Human DNA
C 560	23.4	33.0	190122	9	AC019341	Homo sapi	C 633	23.2	32.7	79726	2	AC095616	AC095616 Rattus no
C 561	23.4	33.0	191924	2	AC091440	Homo sapi	C 634	23.2	32.7	80680	2	AC097842	AC097842 Rattus no
562	23.4	33.0	199745	2	AL671871	Mus muscu	C 635	23.2	32.7	85378	2	ALJ56577	ALJ56577 Homo sapi
C 563	23.4	33.0	201050	1	AL646064	Ralstonia	C 636	23.2	32.7	96332	9	CNS07E66	ALJ56079 Human chr
564	23.4	33.0	202099	2	AC098528	Rattus no	C 637	23.2	32.7	102311	2	AC005377	AC005377 Homo sapi
565	23.4	33.0	202152	2	AC095577	Rattus no	C 638	23.2	32.7	102375	2	AC0205042	AC0205042 Homo sapi
C 566	23.4	33.0	206818	9	AF195953	Homo sapi	C 639	23.2	32.7	103980	9	ALJ54893	ALJ54893 Human DNA
C 567	23.4	33.0	209519	9	AC008397	Homo sapi	C 640	23.2	32.7	110300	2	AC020957	AC020957 Mus muscu
C 568	23.4	33.0	216050	1	AL646076	Ralstonia	C 641	23.2	32.7	111768	9	HS875J18	HS875J18 Human DNA
C 569	23.4	33.0	232156	3	AE003819	Drosophill	C 642	23.2	32.7	123530	2	ALJ39110	ALJ39110 Human DNA
570	23.4	33.0	260910	3	AE003831	Drosophill	C 643	23.2	32.7	132444	9	ALJ590105	ALJ590105 Homo sapi
C 571	23.2	32.7	141	6	AF8950	Sequence	C 644	23.2	32.7	134156	9	ALJ53709	ALJ53709 Human DNA
C 572	23.2	32.7	624	14	AF005102	Hepatitis	C 645	23.2	32.7	134213	9	ALJ57083	ALJ57083 Human DNA
573	23.2	32.7	639	33	AC037031	Giardia i	C 646	23.2	32.7	134570	9	CNS05TEV	ALJ57083 Human chr
574	23.2	32.7	650	9	HS4324173	Homo sapi	C 647	23.2	32.7	134570	9	AF205589	AF205589 Human chr
575	23.2	32.7	687	9	HS4331501	Homo sapi	C 648	23.2	32.7	138929	2	AC011868	AC011868 Homo sapi
576	23.2	32.7	785	33	AC075720	Giardia i	C 649	23.2	32.7	144015	2	ALJ357144	ALJ357144 Homo sapi
577	23.2	32.7	800	33	AC029301	Giardia i	C 650	23.2	32.7	146249	2	ALJ359826	ALJ359826 Homo sapi
578	23.2	32.7	829	33	AC070180	Giardia i	C 651	23.2	32.7	146547	9	HS11B24	AL022394 Human DNA
C 579	23.2	32.7	855	33	AC058026	Giardia i	C 652	23.2	32.7	148181	9	AC083867	AC083867 Homo sapi
C 580	23.2	32.7	932	33	AC071417	Giardia i	C 653	23.2	32.7	149341	9	AC068451	AC068451 Homo sapi
C 581	23.2	32.7	949	33	AC041451	Giardia i	C 654	23.2	32.7	150179	2	AC034213	AC034213 Homo sapi
582	23.2	32.7	963	6	AX047849	Sequence	C 655	23.2	32.7	150393	2	AL671961	AL671961 Mus muscu
583	23.2	32.7	1009	33	AC086713	Giardia i	C 656	23.2	32.7	150583	2	AC104111	AC104111 Homo sapi
C 584	23.2	32.7	1014	33	AC066408	Giardia i	C 657	23.2	32.7	151097	30	AC083846	AC083846 Homo sapi

658	23.2	32.7	151272	2	AC009763	AC009763 Homo sapi	C 731	23.2	32.7	236113	2	AC023825	AC023825 Homo sapi
C 659	23.2	32.7	152422	2	AC106492	AC106492 Rattus no	C 732	23.2	32.7	239566	9	HSAB03147	AJ003147 Homo sapi
C 660	23.2	32.7	153046	2	AC095531	AC095531 Rattus no	C 733	23	32.4	502	6	AX106414	AX106414 Sequence
C 661	23.2	32.7	153825	2	AC016358	AC016358 Homo sapi	C 734	23	32.4	502	6	AX140705	AX140705 Sequence
C 662	23.2	32.7	154471	9	AC022523	AC022523 Homo sapi	C 735	23	32.4	502	6	AX200565	AX200565 Sequence
C 663	23.2	32.7	154960	2	AC011948	AC011948 Homo sapi	C 736	23	32.4	502	6	AX267221	AX267221 Sequence
C 664	23.2	32.7	155055	2	AC096379	AC096379 Rattus no	C 737	23	32.4	567	9	HSAB36826	AJ336826 Homo sapi
C 665	23.2	32.7	155263	8	AP003224	AP003224 Oryza sat	C 738	23	32.4	569	9	HSAB33684	AJ33684 Homo sapi
C 666	23.2	32.7	156066	2	AC099328	AC099328 Homo sapi	C 739	23	32.4	613	9	HSAB324177	AJ332417 Homo sapi
C 667	23.2	32.7	156823	2	AC107948	AC107948 Homo sapi	C 740	23	32.4	650	9	HSAB32753	AJ332753 Homo sapi
C 668	23.2	32.7	157198	2	AC024082	AC024082 Homo sapi	C 741	23	32.4	651	9	HSAB337560	AJ337560 Homo sapi
C 669	23.2	32.7	157321	9	AC068811	AC068811 Homo sapi	C 742	23	32.4	664	9	HSAB336995	AJ336995 Homo sapi
C 670	23.2	32.7	157812	2	AC055805	AC055805 Homo sapi	C 743	23	32.4	688	9	HSAB337561	AJ337561 Homo sapi
C 671	23.2	32.7	160813	2	AC108513	AC108513 Homo sapi	C 744	23	32.4	698	9	HSAB334999	AJ334999 Homo sapi
C 672	23.2	32.7	160852	2	AC020915	AC020915 Homo sapi	C 745	23	32.4	716	9	HSAB333308	AJ333308 Homo sapi
C 673	23.2	32.7	161459	2	AC044783	AC044783 Homo sapi	C 746	23	32.4	722	9	HSAB336807	AJ336807 Homo sapi
C 674	23.2	32.7	162245	2	AC011008	AC011008 Homo sapi	C 747	23	32.4	756	1	PCB132716	PCB132716 Pseudomon
C 675	23.2	32.7	162592	2	AC074155	AC074155 Mus muscu	C 748	23	32.4	762	9	AF041430	AF041430 Homo sapi
C 676	23.2	32.7	162912	2	HSAC002067	HSAC002067 Human BAC	C 749	23	32.4	784	9	HSAB336341	AJ336341 Homo sapi
C 677	23.2	32.7	163108	2	AC016741	AC016741 Homo sapi	C 750	23	32.4	815	9	HSAB336804	AJ336804 Homo sapi
C 678	23.2	32.7	163455	10	MMU2963303	AJ2963303 Mus muscu	C 751	23	32.4	816	9	HSAB336874	AJ336874 Homo sapi
C 679	23.2	32.7	164008	2	AL359877	AL359877 Human DNA	C 752	23	32.4	1263	1	RCU57653	RCU57653 Pseudomon
C 680	23.2	32.7	164077	2	AC024398	AC024398 Homo sapi	C 753	23	32.4	1287	4	BABCYA1A	BABCYA1A BAC
C 681	23.2	32.7	165159	2	AC068577	AC068577 Homo sapi	C 754	23	32.4	1347	9	BC000936	BC000936 Homo sapi
C 682	23.2	32.7	16518	2	AC007431	AC007431 Homo sapi	C 755	23	32.4	1398	9	HSAB0P501	HSAB0P501 Homo sapi
C 683	23.2	32.7	166892	2	AC009969	AC009969 Homo sapi	C 756	23	32.4	2001	6	AX078490	AX078490 Sequence
C 684	23.2	32.7	168448	9	AC009469	AC009469 Homo sapi	C 757	23	32.4	2100	6	AX098220	AX098220 Sequence
C 685	23.2	32.7	168700	2	AC009115	AC009115 Homo sapi	C 758	23	32.4	3368	8	AF274672	AF274672 Vitis aea
C 686	23.2	32.7	169089	9	AC008751	AC008751 Homo sapi	C 759	23	32.4	3773	1	PSENORC	PSENORC Pseudomonas
C 687	23.2	32.7	169284	2	AC098954	AC098954 Rattus no	C 760	23	32.4	4228	10	AF032970	AF032970 Pseudomon
C 688	23.2	32.7	169950	2	AC084049	AC084049 Homo sapi	C 761	23	32.4	5576	10	W05M8CT2A	W05M8CT2A Mouse MHC c
C 689	23.2	32.7	170724	2	AC021059	AC021059 Homo sapi	C 762	23	32.4	6765	10	MMU38816	MMU38816 Mus musculu
C 690	23.2	32.7	171822	2	AC011603	AC011603 Homo sapi	C 763	23	32.4	10425	1	PDENOC0URF	L02534 Paracoccus
C 691	23.2	32.7	173777	2	AC098116	AC098116 Rattus no	C 764	23	32.4	10464	1	AE004634	AE004634 Pseudomon
C 692	23.2	32.7	175127	2	AC016048	AC016048 Homo sapi	C 765	23	32.4	10528	1	PCB271325	PCB271325 Pseudomon
C 693	23.2	32.7	175493	2	AC020769	AC020769 Homo sapi	C 766	23	32.4	10711	1	AE004489	AE004489 Pseudomon
C 694	23.2	32.7	175631	9	AC023511	AC023511 Homo sapi	C 767	23	32.4	10888	1	U32720	U32720 Haemophilus
C 695	23.2	32.7	176968	9	AC005669	AC005669 Homo sapi	C 768	23	32.4	10951	1	AE005756	AE005756 Caulobact
C 696	23.2	32.7	177241	9	HS402611	AL0232328 Human DNA	C 769	23	32.4	11351	1	AE004510	AE004510 Pseudomon
C 697	23.2	32.7	177339	2	AC107975	AC107975 Homo sapi	C 770	23	32.4	11988	1	AE004477	AE004477 Pseudomon
C 698	23.2	32.7	177402	2	AC007406	AC007406 Homo sapi	C 771	23	32.4	12017	6	E22111	E22111 Aromatic co
C 699	23.2	32.7	179172	2	AC026331	AC026331 Homo sapi	C 772	23	32.4	12654	1	AE007167	AE007167 Mycobacte
C 700	23.2	32.7	180749	2	AC025256	AC025256 Homo sapi	C 773	23	32.4	13610	14	AF188480	AF188480 Macropodi
C 701	23.2	32.7	182441	2	AC108154	AC108154 Homo sapi	C 774	23	32.4	25381	1	SC2H2	AL450289 Streptomy
C 702	23.2	32.7	184547	2	AC074373	AC074373 Homo sapi	C 775	23	32.4	26963	1	SCC105	AL163641 Streptomy
C 703	23.2	32.7	187735	2	AC061979	AC061979 Homo sapi	C 776	23	32.4	27300	1	SCD39	AL132146 Streptomy
C 704	23.2	32.7	192381	2	AC012645	AC012645 Homo sapi	C 777	23	32.4	28951	1	HS1616C2	Z68169 Human DNA s
C 705	23.2	32.7	193050	1	AL646062	AL646062 Ralstonia	C 778	23	32.4	35292	1	MRCY36C7	Z82098 Mycobacte
C 706	23.2	32.7	193101	2	AC009561	AC009561 Homo sapi	C 779	23	32.4	37186	1	MSGY244	AD000003 Mycobacte
C 707	23.2	32.7	193829	9	AC012154	AC012154 Homo sapi	C 780	23	32.4	38400	1	SC4H2	AL022268 Streptomy
C 708	23.2	32.7	194804	2	AL358253	AL358253 Homo sapi	C 781	23	32.4	39726	1	SCB11	AL512944 Streptomy
C 709	23.2	32.7	195378	2	AL133410	AL133410 Human DNA	C 782	23	32.4	41782	1	SCG11A	AL132210 Streptomy
C 710	23.2	32.7	195955	2	AC079800	AC079800 Homo sapi	C 783	23	32.4	56917	1	AME16952	Y16952 Amycolatops
C 711	23.2	32.7	196050	1	AL646058	AL646058 Ralstonia	C 784	23	32.4	58707	2	AC100810	AC100810 Homo sapi
C 712	23.2	32.7	196787	2	AC104134	AC104134 Homo sapi	C 785	23	32.4	70954	2	AC104916	AC104916 Mus muscu
C 713	23.2	32.7	197445	2	AC040970	AC040970 Homo sapi	C 786	23	32.4	72383	2	AC027746	AC027746 Homo sapi
C 714	23.2	32.7	197926	2	AC010550	AC010550 Homo sapi	C 787	23	32.4	75695	2	AC025345	AC025345 Homo sapi
C 715	23.2	32.7	198402	2	AC026373	AC026373 Homo sapi	C 788	23	32.4	83373	8	AB017064	AB017064 Arabidops
C 716	23.2	32.7	200925	2	AC009090	AC009090 Homo sapi	C 789	23	32.4	86441	1	AL390762	AL390762 Homo sapi
C 717	23.2	32.7	202540	9	AC002524	AC002524 Homo sapi	C 790	23	32.4	86896	1	RCU57682	U57682 Rhodobacter
C 718	23.2	32.7	204058	2	AC048337	AC048337 Homo sapi	C 791	23	32.4	95808	2	AF214636	AF214636 Homo sapi
C 719	23.2	32.7	204062	2	AC026333	AC026333 Homo sapi	C 792	23	32.4	100000	2	AP000518	AP000518 Homo sapi
C 720	23.2	32.7	204653	10	AC005302	AL604066 Mus muscu	C 793	23	32.4	101369	2	AC096489	AC096489 Rattus no
C 721	23.2	32.7	205832	2	AL604066	AL604066 Mus muscu	C 794	23	32.4	104160	2	AC094039	AC094039 Rattus no
C 722	23.2	32.7	205912	2	AC044847	AC044847 Mus muscu	C 795	23	32.4	111084	2	AC006486	AC006486 Homo sapi
C 723	23.2	32.7	207050	1	AL646063	AL646063 Ralstonia	C 796	23	32.4	113255	9	AP000345	AP000345 Homo sapi
C 724	23.2	32.7	207425	2	AC060790	AC060790 Homo sapi	C 797	23	32.4	114194	2	AC093200	AC093200 Homo sapi
C 725	23.2	32.7	210036	2	AC009782	AC009782 Homo sapi	C 798	23	32.4	117863	2	AP004550	AP004550 Homo sapi
C 726	23.2	32.7	213721	2	HS172820	AL022323 Human DNA	C 799	23	32.4	120194	9	AL355474	AL355474 Human DNA
C 727	23.2	32.7	218547	2	AL607024	AL607024 Mus muscu	C 800	23	32.4	123436	9	AC009872	AC009872 Homo sapi
C 728	23.2	32.7	219553	2	HSAB12687	AJ312687 Homo sapi	C 801	23	32.4	138038	2	AL591435	AL591435 Human DNA
C 729	23.2	32.7	220119	10	AC096776	AC096776 Mus muscu	C 802	23	32.4	140108	2	AP004125	AP004125 Oryza sat
C 730	23.2	32.7	233993	2	AC110000	AC110000 Homo sapi	C 803	23	32.4	140452	10	AC006447	AC006447 Mus muscu

804	23	32.4	142776	10	AC006404	AC006404 Mus muscu	c 877	22.8	32.1	1145	1	ECU20815	U20815 Escherichia
c 805	23	32.4	146420	2	AP004621	AP004621 Oryza sat	c 878	22.8	32.1	1346	14	HS1ICP345B	M33700 Herpes simp
c 806	23	32.4	146655	2	HS1120P1.1	HS1120P1.1 Human DNA	c 879	22.8	32.1	1367	14	HS1ICP345C	M33700 Herpes simp
c 807	23	32.4	147657	2	AC016967	AC016967 Homo sapi	c 880	22.8	32.1	1399	14	HS1ICP345A	M33699 Herpes simp
c 808	23	32.4	148054	9	AC026467	AC026467 Homo sapi	c 881	22.8	32.1	1450	1	ECF1MA01	X00981 E. coli fim
c 809	23	32.4	149322	2	AC016039	AC016039 Homo sapi	c 882	22.8	32.1	1635	9	BC000681	BC000681 Homo sapi
c 810	23	32.4	151117	2	AL357128	AL357128 Homo sapi	c 883	22.8	32.1	1785	9	AK025854	AK025854 Homo sapi
c 811	23	32.4	151600	2	AP000346	AP000346 Homo sapi	c 884	22.8	32.1	1794	14	HS1ICP1	M12240 Herpes simp
c 812	23	32.4	151997	2	OSJND1010	AL607102 Oryza sat	c 885	22.8	32.1	2010	10	BC002283	BC002283 Mus muscu
c 813	23	32.4	153483	2	AC068899	AC068899 Mus muscu	c 886	22.8	32.1	2046	10	U00932	U00932 Mus muscu
c 814	23	32.4	153863	2	AC025361	AC025361 Homo sapi	c 887	22.8	32.1	2302	10	BC010516	BC010516 Mus muscu
c 815	23	32.4	156266	8	AP002542	AP002542 Oryza sat	c 888	22.8	32.1	2305	10	AF334736	AF334736 Mus muscu
c 816	23	32.4	157562	2	AC011574	AC011574 Homo sapi	c 889	22.8	32.1	2864	9	AF125253	AF125253 Homo sapi
c 817	23	32.4	158673	2	AC095235	AC095235 Rattus no	c 890	22.8	32.1	3143	9	BC003089	BC003089 Homo sapi
c 818	23	32.4	162248	2	AC025154	AC025154 Homo sapi	c 891	22.8	32.1	3301	9	HSMB02123	HSMB02123 Homo sapi
c 819	23	32.4	167014	2	AP004706	AP004706 Oryza sat	c 892	22.8	32.1	3395	14	OV049979	OV049979 Oryza sat
c 820	23	32.4	167619	2	AL671859	AL671859 Homo sapi	c 893	22.8	32.1	3418	9	BC004181	BC004181 Homo sapi
c 821	23	32.4	167966	2	AC093398	AC093398 Bos tauru	c 894	22.8	32.1	3423	9	BC008733	BC008733 Homo sapi
c 822	23	32.4	168239	9	AC007663	AC007663 Homo sapi	c 895	22.8	32.1	3448	9	HSMB02882	HSMB02882 Homo sapi
c 823	23	32.4	169027	2	AC099282	AC099282 Rattus no	c 896	22.8	32.1	4672	9	HSSERC48	HSSERC48 Homo sapien
c 824	23	32.4	169356	2	AL671277	AL671277 Homo sapi	c 897	22.8	32.1	10765	1	AE004555	AE004555 Pseudomon
c 825	23	32.4	169599	9	AL512665	AL512665 Human DNA	c 898	22.8	32.1	10965	1	AE002004	AE002004 Deinococc
c 826	23	32.4	170408	2	AL645924	AL645924 Homo sapi	c 899	22.8	32.1	11313	1	AE000502	AE000502 Escherich
c 827	23	32.4	170650	2	AC094783	AC094783 Rattus no	c 900	22.8	32.1	14466	1	AE005662	AE005662 Escherich
c 828	23	32.4	172592	2	AC094231	AC094231 Rattus no	c 901	22.8	32.1	15335	1	AE007037	AE007037 Mycobacte
c 829	23	32.4	172613	2	AL365502	AL365502 Homo sapi	c 902	22.8	32.1	15576	1	AE007135	AE007135 Mycobacte
c 830	23	32.4	172718	2	AC096649	AC096649 Homo sapi	c 903	22.8	32.1	22947	1	MTCY4C12	MTCY4C12 Streptomy
c 831	23	32.4	174555	2	AC067739	AC067739 Homo sapi	c 904	22.8	32.1	26500	1	SC9H11	SC9H11 Streptomy
c 832	23	32.4	174840	2	AC006549	AC006549 Homo sapi	c 905	22.8	32.1	29084	3	AC022543	AC022543 Homo sapi
c 833	23	32.4	176463	2	AC012149	AC012149 Homo sapi	c 906	22.8	32.1	29120	3	AF016446	AF016446 Caenorhab
c 834	23	32.4	176552	2	AC024622	AC024622 Homo sapi	c 907	22.8	32.1	30000	9	HSAT272265	HSAT272265 Homo sapi
c 835	23	32.4	176628	2	AC097031	AC097031 Rattus no	c 908	22.8	32.1	30561	1	SC1E2	SC1E2 Streptomy
c 836	23	32.4	182453	2	AC091714	AC091714 Papio cyn	c 909	22.8	32.1	35716	9	AC092302	AC092302 Homo sapi
c 837	23	32.4	183976	9	AL356056	AL356056 Human DNA	c 910	22.8	32.1	36307	9	HS36BD1	HS36BD1 Human DNA s
c 838	23	32.4	184929	9	AC058790	AC058790 Homo sapi	c 911	22.8	32.1	37730	1	SC8D9	SC8D9 Streptomy
c 839	23	32.4	185167	9	AC009077	AC009077 Homo sapi	c 912	22.8	32.1	38681	9	AC004232	AC004232 Streptomy
c 840	23	32.4	185327	9	AC007224	AC007224 Homo sapi	c 913	22.8	32.1	39009	1	MTCY164	MTCY164 Mycobacteri
c 841	23	32.4	185755	2	AC084273	AC084273 Mus muscu	c 914	22.8	32.1	39150	1	SC27G11	SC27G11 Streptomy
c 842	23	32.4	186656	2	AL592143	AL592143 Homo sapi	c 915	22.8	32.1	42348	2	AC102066	AC102066 Mus muscu
c 843	23	32.4	187175	2	AC104579	AC104579 Homo sapi	c 916	22.8	32.1	49239	2	AR007269	AR007269 Sequence
c 844	23	32.4	189709	9	AL160275	AL160275 Human DNA	c 917	22.8	32.1	50341	6	AR091570	AR091570 Sequence
c 845	23	32.4	189806	9	AC021382	AC021382 Homo sapi	c 918	22.8	32.1	50341	6	AR091570	AR091570 Sequence
c 846	23	32.4	191535	2	AC022505	AC022505 Homo sapi	c 919	22.8	32.1	52297	7	ARI48205	ARI48205 Sequence
c 847	23	32.4	196037	2	AL607066	AL607066 Mus muscu	c 920	22.8	32.1	52297	6	MLC6A	MLC6A Mycobacteri
c 848	23	32.4	196038	2	AL161451	AL161451 Homo sapi	c 921	22.8	32.1	53425	1	EA067194	EA067194 Enterobacte
c 849	23	32.4	198050	1	AL646061	AL646061 Ralstonia	c 922	22.8	32.1	58996	1	AB034704	AB034704 Ralstonia
c 850	23	32.4	199414	2	AC084125	AC084125 Homo sapi	c 923	22.8	32.1	60966	9	AC003030	AC003030 Homo sapi
c 851	23	32.4	203612	2	AC098208	AC098208 Rattus no	c 924	22.8	32.1	65698	2	AC011258	AC011258 Homo sapi
c 852	23	32.4	212706	2	AC073153	AC073153 Mus muscu	c 925	22.8	32.1	67166	2	AC012546	AC012546 Homo sapi
c 853	23	32.4	213045	2	AC093640	AC093640 Homo sapi	c 926	22.8	32.1	77457	1	AF210249	AF210249 Streptomy
c 854	23	32.4	215052	2	AL590627	AL590627 Homo sapi	c 927	22.8	32.1	84077	9	AL157371	AL157371 Human DNA
c 855	23	32.4	216408	2	AC092466	AC092466 Homo sapi	c 928	22.8	32.1	84797	9	AL356778	AL356778 Human DNA
c 856	23	32.4	217992	2	AC040162	AC040162 Homo sapi	c 929	22.8	32.1	95073	2	AC007272	AC007272 Homo sapi
c 857	23	32.4	222605	9	AC010973	AC010973 Homo sapi	c 930	22.8	32.1	104131	2	AC094820	AC094820 Rattus no
c 858	23	32.4	229700	2	AC073777	AC073777 Mus muscu	c 931	22.8	32.1	108711	9	AC006037	AC006037 Homo sapi
c 859	23	32.4	236491	2	AC099290	AC099290 Rattus no	c 932	22.8	32.1	108845	1	U66917	U66917 Pseudomonas
c 860	23	32.4	349980	6	AX120085	AX120085 Sequence	c 933	22.8	32.1	110000	2	AL354714_3	AL354714_3 Continuation (4 of
c 861	23	32.4	349980	6	AX127144	AX127144 Sequence	c 934	22.8	32.1	113182	2	AC008894	AC008894 Homo sapi
c 862	22.8	32.1	294	1	PAU15326	U15326 Pseudomonas	c 935	22.8	32.1	115049	2	AC0073746	AC0073746 Mus muscu
c 863	22.8	32.1	34	33	AC040774	AC040774 Giardia i	c 936	22.8	32.1	119750	9	HSJD1989D7	HSJD1989D7 Human DNA
c 864	22.8	32.1	520	8	HDY17093	HDY17093 Hyponyces d	c 937	22.8	32.1	120533	9	AL353717	AL353717 Human DNA
c 865	22.8	32.1	549	1	AF206650	AF206650 Escherich	c 938	22.8	32.1	123661	9	AC004518	AC004518 Homo sapi
c 866	22.8	32.1	549	1	AF206652	AF206652 Escherich	c 939	22.8	32.1	125507	9	AL450336	AL450336 Human DNA
c 867	22.8	32.1	549	1	AF206653	AF206653 Escherich	c 940	22.8	32.1	125638	9	AC004706	AC004706 Homo sapi
c 868	22.8	32.1	549	1	AF206658	AF206658 Escherich	c 941	22.8	32.1	128119	9	AC008101	AC008101 Homo sapi
c 869	22.8	32.1	549	1	AF206659	AF206659 Escherich	c 942	22.8	32.1	132244	2	AC093178	AC093178 Oryza sat
c 870	22.8	32.1	642	9	HS435297	HS435297 Homo sapi	c 943	22.8	32.1	137296	2	AC074162	AC074162 Mus muscu
c 871	22.8	32.1	824	14	AF251159	AF251159 Human bet	c 944	22.8	32.1	142839	9	AL356218	AL356218 Human DNA
c 872	22.8	32.1	832	1	HS4329121	HS4329121 Homo sapi	c 945	22.8	32.1	143250	9	AC005997	AC005997 Homo sapi
c 873	22.8	32.1	853	1	ECOP1LAA	M27603 E.coli pili	c 946	22.8	32.1	144219	8	AP004194	AP004194 Oryza sat
c 874	22.8	32.1	855	6	AX079023	AX079023 Sequence	c 947	22.8	32.1	145356	9	AL513366	AL513366 Homo sapi
c 875	22.8	32.1	896	9	HS4343354	AJ343354 Homo sapi	c 948	22.8	32.1	145456	9	AL513366	AL513366 Human DNA
c 876	22.8	32.1	947	14	AF251158	AF251158 Human bet	c 949	22.8	32.1	147146	2	AP003316	AP003316 Oryza sat

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951	22.8	32.1	149805	9	CNS07861	AL589168 Human chr
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955	22.8	32.1	160555	9	AC064874	AC064874 Homo sapi
956	22.8	32.1	161798	2	AC068062	AC068062 Homo sapi
957	22.8	32.1	163344	2	AC060233	AC060233 Homo sapi
958	22.8	32.1	163924	2	AL162592	AL162592 Homo sapi
959	22.8	32.1	165799	2	AL135879	AL135879 Human DNA
960	22.8	32.1	166050	1	AL646085	AL646085 Ralstonia
961	22.8	32.1	166118	2	OSJN00208	AL663005 Oryza sat
962	22.8	32.1	166336	9	AL445467	AL445467 Human DNA
963	22.8	32.1	166832	9	AF070718	AF070718 Homo sapi
964	22.8	32.1	168497	2	AC092410	AC092410 Bos tauru
965	22.8	32.1	168764	1	AP002569	AP002569 Escherich
966	22.8	32.1	169223	2	AL353675	AL353675 Homo sapi
967	22.8	32.1	169334	2	AC025406	AC025406 Homo sapi
968	22.8	32.1	170632	9	AL136321	AL136321 Human DNA
969	22.8	32.1	171087	9	AC073584	AC073584 Homo sapi
970	22.8	32.1	171751	2	AC094037	AC094037 Rattus no
971	22.8	32.1	172033	9	AL136131	AL136131 Human DNA
972	22.8	32.1	172862	2	AL645796	AL645796 Homo sapi
973	22.8	32.1	173039	2	CNS01DVB	AL133523 Human chr
974	22.8	32.1	174636	2	AC027778	AC027778 Homo sapi
975	22.8	32.1	176268	2	AL591001	AL591001 Homo sapi
976	22.8	32.1	177344	9	AL356953	AL356953 Human DNA
977	22.8	32.1	181141	2	AC093621	AC093621 Homo sapi
978	22.8	32.1	181609	9	AC079385	AC079385 Homo sapi
979	22.8	32.1	182617	9	AC007731	AC007731 Homo sapi
980	22.8	32.1	183044	2	AC079827	AC079827 Homo sapi
981	22.8	32.1	184043	2	AC092835	AC092835 Homo sapi
982	22.8	32.1	185975	2	AC104581	AC104581 Homo sapi
983	22.8	32.1	192592	9	AC005500	AC005500 Homo sapi
984	22.8	32.1	192720	9	AC016830	AC016830 Homo sapi
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986	22.8	32.1	196272	2	AC026675	AC026675 Homo sapi
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988	22.8	32.1	197144	9	AC073347	AC073347 Homo sapi
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991	22.8	32.1	200000	2	AC006294	AC006294 Homo sapi
992	22.8	32.1	200329	10	AC078911	AC078911 Mus muscu
993	22.8	32.1	200885	2	AC012460	AC012460 Homo sapi
994	22.8	32.1	203591	1	AC007156	AC007156 Homo sapi
995	22.8	32.1	204050	9	AL646070	AL646070 Ralstonia
996	22.8	32.1	206187	2	AC021172	AC021172 Homo sapi
997	22.8	32.1	206517	2	AP003407	AP003407 Oryza sat
998	22.8	32.1	212335	2	AL356275	AL356275 Homo sapi
999	22.8	32.1	216585	2	AP002387	AP002387 Homo sapi
1000	22.8	32.1	218634	2	AC106791	AC106791 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS HSOPRM1 305 bp DNA linear PRI 02-DEC-1997
DEFINITION Homo sapiens mu opioid receptor (OPRM1) gene, partial cds, exon 1.
ACCESSION AF024515.1 GI:2655101
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 305)
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A.
and Uhl, G.R.
Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment

JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 9413928
REFERENCE 2 (bases 1 to 305)
AUTHORS Bare, L.A., Mansson, E. and Yang, D.
TITLE Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain
JOURNAL FEBS Lett. 354 (2), 213-216 (1994)
MEDLINE 95046336
REFERENCE 3 (bases 1 to 305)
AUTHORS Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M., Linnola, M. and Goldman, D.
TITLE Mu opioid receptor gene variants: lack of association with alcohol dependence
JOURNAL Mol. Psychiatry 2 (6), 490-494 (1997)
MEDLINE 98060615
REFERENCE 4 (bases 1 to 305)
AUTHORS Bergen, A.W., Kokoszka, J. and Goldman, D.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1997) Neurogenetics, NIMH/NIH, 12501 Washington Avenue, Rockville, MD 20852, USA
COMMENT 134 US Caucasian and North American Indian chromosomes were directly sequenced at the OPRM1 locus, 5'UTR and Exon 1.
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1994]"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCTGGGCGGAGAGACACACCTGT 60
LOCUS 153 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCGACCTGGGCGGAGAGACACACCTGT 212
OY 61 GCCCTCGGACC 71
Db 213 GCCCTCGGACC 223

RESULT 2
G53082/c 520 bp DNA linear STS 30-MAR-2000
LOCUS SHCC-84785 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G53082
ACCESSION G53082.1 GI:5224409
VERSION STS.
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Olivier,M., and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished

COMMENT Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: TTTACTCTCCCTCTTTCATCTC
Primer B: ACTTGTCACCTTAGATGGCAAC
STS size: 307

PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
AmpliTaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCTGGGCGGAGAGACACACCTGT 60
LOCUS 355 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCGACCTGGGCGGAGAGACACACCTGT 296
OY 61 GCCCTCGGACC 71
Db 295 GCCCTCGGACC 285

RESULT 3
AF286024 1203 bp mRNA linear PRI 03-AUG-2000
LOCUS Macaca mulatta mu opioid receptor mRNA, complete cds.
DEFINITION AF286024
ACCESSION AF286024
VERSION AF286024.1 GI:9664878
KEYWORDS
SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Miller,G.M. and Madras,B.K.
TITLE Cloning of the Macaca mulatta mu opioid receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1203)
AUTHORS Miller,G.M. and Madras,B.K.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2000) Neurochemistry, New England Regional
Primate Research Center, Harvard Medical School, One Pine Hill
Drive, Southborough, MA 01772, USA

FEATURES
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CTMSVDRIAYVCHPKALDERTPRNAKINVCNMLISSAIGLUPPMFATTKYRGSD
CLTFESHPSWTEMLKICVFIFALPVLITVCGILMLILRLKSVMLSGSEKDRN
LRRTRNVLVAVFIIICMTPIYIVIKALVLPETFTQVSMHFCIALGYNSCLN
PVLVAFIDENFKRCFRFCIPTSSNIPOONSTRIRONTBDHPSTANTVDRNTNHOENTL
EAETAPLP"

BASE COUNT 299 a 350 c 242 g 312 t
ORIGIN
Query Match 100.0%; Score 71; DB 9; Length 1203;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCTGGGCGGAGAGACACACCTGT 60
LOCUS 116 GCAACCTGCGACCCATGCGGTCCGAGAACCGACCGACCGACCTGGGCGGAGAGACACACCTGT 175
OY 61 GCCCTCGGACC 71
Db 176 GCCCTCGGACC 186

RESULT 4
AY038989 1399 bp mRNA linear PRI 15-JUL-2001
LOCUS Macaca fascicularis mu-opioid receptor mRNA, complete cds.
DEFINITION AY038989
ACCESSION AY038989.1 GI:14718771
VERSION
KEYWORDS
SOURCE crab-eating macaque.

ORGANISM Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE 1 (bases 1 to 1399)
AUTHORS Miller, G.M. and Madras, B.K.
JOURNAL Cloning of the Macaca fascicularis mu opioid receptor
TITLE Unpublished
REFERENCE 2 (bases 1 to 1399)
AUTHORS Miller, G.M. and Madras, B.K.
TITLE Direct Submission
SUBMITTED (07-JUN-2001) Neurochemistry, New England Primate
Research Center, Harvard Medical School, One Pine Hill Drive,
Southborough, MA 01772, USA
LOCATION/Qualifiers
1. 1399
FEATURES
source
CDS
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
80..1282
/note="G-protein-linked receptor"
/product="mu-opioid receptor"
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/db_xref="GI:14718772"
/translation="MDSSAVPTNASCNTDALAHSSGSPAPSGSWVNLSHLDGNTSDP
CGPNRTDLGGRSLCPPTGSPSMITAITMALYSIVCYVGLGNFLVWYVIRYRK
PATNIYIFNLALADALVSTLPEOSVNYLMGTPTLCKIVISIDYNNFTSFTL
CMYSVDRIYAVCHPVKALDFRPNRAKIIINVCNWLSSAIGLPMVMTATKYRQSID
CUTLFSHPWYENLTKICVEIFAEIPVLIITVCGMLILKSVRMISGSKEDRN
LRITRMVLYVAVFLICWTPPHIYVITKALVTIETTTQIVSMHFCIALGYNSCLN
PVLVAFIDENFKRCFRFCIPPTSSNIEQNSRIRIQRNDRHSTANTVDRTHOLENT
EAETAPLP"
BASE COUNT 342 a 411 c 291 g 355 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
Db 195 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 254
OY 61 GCCCTCCGACC 71
Db 255 GCCCTCCGACC 265
RESULT 5
LOCUS ARI06017 1610 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6103492.
ACCESSION ARI06017
VERSION ARI06017.1 GI:12820082
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1610)
AUTHORS Yu, L.
TITLE Polynucleotide encoding mu opioid receptor
JOURNAL Patent: US 6103492-A 7 15-AUG-2000.
FEATURES
source
1. 1610
/organism="unknown"
BASE COUNT 384 a 467 c 359 g 400 t
ORIGIN
Query Match 100.0%; Score 71; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
Db 195 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGAGACAGCCTGT 254
OY 61 GCCCTCCGACC 71
Db 255 GCCCTCCGACC 265
RESULT 5
LOCUS ARI06017 1610 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6103492.
ACCESSION ARI06017
VERSION ARI06017.1 GI:12820082
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1610)
AUTHORS Yu, L.
TITLE Polynucleotide encoding mu opioid receptor
JOURNAL Patent: US 6103492-A 7 15-AUG-2000.
FEATURES
source
1. 1610
/organism="unknown"
BASE COUNT 384 a 467 c 359 g 400 t
ORIGIN

Db 354 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGAGACAGCCTGT 413
OY 61 GCCCTCCGACC 71
Db 414 GCCCTCCGACC 424
RESULT 6
LOCUS HUMOPI01DA 1610 bp mRNA linear PRI 03-AUG-1995
DEFINITION Homo sapiens opioid receptor mRNA, complete cds.
ACCESSION L29301
VERSION L29301.1 GI:459831
KEYWORDS opioid receptor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1610)
AUTHORS Mestek, A., Hurley, J.H., Bye, L.S., Campbell, A.D., Chen, Y., Tian, M.,
Liu, J., Schulman, H. and Yu, L.
TITLE The human mu opioid receptor: modulation of functional
desensitization by calcium/calmodulin-dependent protein kinase and
protein kinase C
JOURNAL J. Neurosci. 15 (3), 2396-2406 (1995)
MEDLINE 95198115
FEATURES
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1. 1610
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="caudate nucleus"
/dev_stage="adult"
/tissue_lib="Clontech lambda gtl1"
239..1441
/note="putative"
/codon_start=1
/product="opioid receptor"
/protein_id="AAA73958.1"
/db_xref="GI:459832"
/translation="MDSSAVPTNASCNTDALAHSSGSPAPSGSWVNLSHLDGNTSDP
CGPNRTDLGGRSLCPPTGSPSMITAITMALYSIVCYVGLGNFLVWYVIRYRK
PATNIYIFNLALADALVSTLPEOSVNYLMGTPTLCKIVISIDYNNFTSFTL
CMYSVDRIYAVCHPVKALDFRPNRAKIIINVCNWLSSAIGLPMVMTATKYRQSID
CUTLFSHPWYENLTKICVEIFAEIPVLIITVCGMLILKSVRMISGSKEDRN
LRITRMVLYVAVFLICWTPPHIYVITKALVTIETTTQIVSMHFCIALGYNSCLN
PVLVAFIDENFKRCFRFCIPPTSSNIEQNSRIRIQRNDRHSTANTVDRTHOLENT
EAETAPLP"
BASE COUNT 384 a 467 c 359 g 400 t
ORIGIN
Query Match 100.0%; Score 71; DB 9; Length 1610;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGAGACAGCCTGT 60
Db 354 GCAACCTGTCGACCATGCGGTCCGAACCGACCGACCTGGCGGAGAGAGAGACAGCCTGT 413
OY 61 GCCCTCCGACC 71
Db 414 GCCCTCCGACC 424
RESULT 7
LOCUS ALI36444/c 96310 bp DNA linear PRI 06-NOV-2000
DEFINITION Human DNA sequence from clone RP3-366F13 on chromosome 6 Contains
ESTs, STSS, GSSs and a Cpg island. contains the OPRM1 gene encoding
opioid receptor mu 1, complete sequence.
ACCESSION ALI36444
VERSION ALI36444.15 GI:9944119
KEYWORDS HTG; Cpg island; mu 1; opioid receptor; OPRM1.


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misc_feature      15644..16491
                    /note="match: GSS: Em:AQ748251"
repeat_region     16425..16537
                    /note="LIM48 repeat: matches 6176..6289 of consensus"
repeat_region     16824..17072
                    /note="AluSq repeat: matches 1..300 of consensus"
misc_feature      complement(17700..18193)
                    /gene="OPRM1"
misc_feature      /note="match: GSS: Em:AQ777968"
                    complement(17761..18197)
                    /gene="OPRM1"
repeat_region     18009..18044
                    /note="match: GSS: Em:AQ805239"
                    /gene="OPRM1"
misc_feature      18162..18373
                    /note="9 copies 4 mer tgtt 97% conserved"
repeat_region     18505..18548
                    /note="match: STS: Em:L30053"
repeat_region     18992..19300
                    /note="11 copies 4 mer gtgt 77% conserved"
repeat_region     20685..20734
                    /note="AluY repeat: matches 1..307 of consensus"
repeat_region     21426..21739
                    /note="L2 repeat: matches 2655..2705 of consensus"
                    /note="AluY repeat: matches 1..311 of consensus"
                    complement(22272..22843)
misc_feature      /gene="OPRM1"
                    /note="match: GSS: Em:AQ533470"
                    complement(22355..22858)
                    /gene="OPRM1"
repeat_region     22427..22547
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repeat_region     22375..22788
                    /note="MER69 repeat: matches 489..614 of consensus"
repeat_region     22769..23087
                    /note="MER69 repeat: matches 662..893 of consensus"
repeat_region     23088..23246
                    /note="MER69 repeat: matches 1991..2295 of consensus"
repeat_region     23247..23438
                    /note="FRAM repeat: matches 2..159 of consensus"
misc_feature      23763..24232
                    /note="MER69 repeat: matches 2295..2490 of consensus"
                    /note="match: GSS: Em:AQ793055"
repeat_region     24067..24372
                    /note="AluJb repeat: matches 1..299 of consensus"
repeat_region     24601..25199
                    /note="L2 repeat: matches 1142..1818 of consensus"
repeat_region     25225..25512

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Best Local Similarity 100.0%; Pred. No. 9,4e-11;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCTGTCGCGACGATGGCTCGAAGCGACGCTGGGGGAGAGACGCGCT 60
Db 63301 GCACCTGTCGCGACGATGGCTCGAAGCGACGCTGGGGGAGAGACGCGCT 63242

QY 61 GCCCTCCGACC 71
Db 63241 GCCCTCCGACC 63231

RESULT 8
AC027439          182048 bp   DNA      linear   HTG 14-JUN-2000
LOCUS            Homo sapiens chromosome 6 clone RP11-30607 map 6, WORKING DRAFT
DEFINITION       SEQUENCE: 18 unordered pieces.
ACCESSION       AC027439
VERSION         AC027439.2   GI: 8516101
KEYWORDS        HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE          human.
ORGANISM        Homo sapiens
                 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE
AUTHORS          1 (bases 1 to 182048)
TITLE            Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL          Homo sapiens chromosome 6, clone RP11-30607
REFERENCE        Unpublished
AUTHORS          2 (bases 1 to 182048)
                 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
                 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
                 Campiano,A., Castle,A., Choelel,Y., Colangelo,M., Collins,S.,
                 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,D.S.,
                 Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
                 Galagan,J., Gardyna,S., Glnde,S., Goylete,M., Graham,L.,
                 Grand-Pierre,N., Grant,G., Hagos,B., Healdor,A., Horton,L.,
                 Howland,J.C., Illey,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
                 Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
                 Levine,R., Lien,C., Liu,G., Locke,K., Macdonald,P., Margus,N.,
                 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
                 Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
                 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
                 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
                 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
                 Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
                 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggilio,J.,
                 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                 Direct Submission
                 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
                 Research, 320 Charles Street, Cambridge, MA 02141, USA
                 On Jun 14, 2000 this sequence version replaced gi:7342168.
                 All repeats were identified using RepeatMasker:
                 Smit,A.F.A. & Green, P. (1996-1997)
                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                 ----- Genome Center
                 Center: Whitehead Institute/ MIT Center for Genome Research
                 Center code: MIBR
                 Web site: http://www-seq.wi.mit.edu
                 Contact: sequence.submissions@genome.wi.mit.edu
                 ----- Project Information
                 Center project name: L8135
                 Center clone name: 306.O.7
                 ----- Summary Statistics
                 Sequencing vector: M13; M7815; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.960731
                 Consensus quality: 172491 bases at least Q40
                 Consensus quality: 177577 bases at least Q30
                 Consensus quality: 179485 bases at least Q20
                 Insert size: 188000; agarose-fp
                 Insert size: 180348; sum-of-contigs
                 Quality coverage: 4.4 in Q20 bases; agarose-fp
                 Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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                 * NOTE: This is a 'working draft' sequence. It currently
                 * consists of 18 contigs. The true order of the pieces
                 * is not known and their order in this sequence record is
                 * arbitrary. Gaps between the contigs are represented as
                 * runs of N, but the exact sizes of the gaps are unknown.
                 * This record will be updated with the finished sequence
                 * as soon as it is available and the accession number will
                 * be preserved.
                 *
                 1 1047: contig of 1047 bp in length
                 * 1048 1147: gap of 100 bp
                 * 1148 1354: contig of 207 bp in length
                 * 1355 1454: gap of 100 bp
                 * 1455 3155: contig of 1701 bp in length
                 * 3156 3255: gap of 100 bp
                 * 3256 6573: contig of 3318 bp in length
                 * 6574 6673: gap of 100 bp
                 * 6674 9233: contig of 2560 bp in length
                 * 9234 9333: gap of 100 bp
                 * 9334 12513: contig of 3180 bp in length
                 * 12514 12613: gap of 100 bp

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* 12614 18852: contig of 6239 bp in length
* 18853 18952: gap of 100 bp
* 18953 24896: contig of 5944 bp in length
* 24897 24996: gap of 100 bp
* 24997 32904: contig of 7908 bp in length
* 32905 33004: gap of 100 bp
* 33005 41063: contig of 8059 bp in length
* 41064 41163: gap of 100 bp
* 41164 49312: contig of 8149 bp in length
* 49313 49412: gap of 100 bp
* 49413 60412: contig of 11000 bp in length
* 60413 60512: gap of 100 bp
* 60513 73244: contig of 12732 bp in length
* 73245 73344: gap of 100 bp
* 73345 88021: contig of 14677 bp in length
* 88022 88121: gap of 100 bp
* 88122 105702: contig of 17581 bp in length
* 105703 105802: gap of 100 bp
* 105803 131166: contig of 25364 bp in length
* 131167 131266: gap of 100 bp
* 131267 158770: contig of 27504 bp in length
* 158771 158870: gap of 100 bp
* 158871 182048: contig of 23178 bp in length.

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FEATURES

source

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/db_xref="taxon:9606"
/chromosome="6"
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/clone.lib="RPCT-11 Human Male BAC"
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1148..1354
/note="assembly-fragment"
clone_end:SP6
vector_side:left"
1455..3155
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3236..6573
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6674..9233
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9334..12513
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18953..24896
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24997..32904
/note="assembly-fragment"
33005..41063
/note="assembly-fragment"
41164..49312
/note="assembly-fragment"
49413..60412
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60513..73244
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73345..88021
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105803..131166
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131267..158770
/note="assembly-fragment"
158871..182048
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BASE COUNT 55404 a 35093 c 35419 g 54431 t 1701 others
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Query Match 100.0%; Score 71; DB 2; Length 182048;

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Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCCGAACCGACCGACCTGGCGGAGAGACACCTGT 60
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Db 75837 GCAACCTGTCGACCATCGGTCCGAACCGACCGACCGACCTGGCGGAGAGACACCTGT 75896
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QY 61 GCCCTCCGAC 71
|||||

Db 75897 GCCCTCCGAC 75907

RESULT 9

AC021745/c

LOCUS

DEFINITION Homo sapiens chromosome 11 clone RP11-339D1 map 11, WORKING DRAFT

SEQUENCE, 9 unordered pieces.

AC021745

AC021745.3 GI:7408033

VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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JOURNAL

REFERENCE

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TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 4, 2000 this sequence version replaced gi:6910869.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L6050
Center clone name: 339.D.1

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175126 bases at least Q40
Consensus quality: 178423 bases at least Q30
Consensus quality: 179878 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 181583; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 547: contig of 547 bp in length
548 647: gap of 100 bp
648 2304: contig of 1657 bp in length
2305 2404: gap of 100 bp
2405 4706: contig of 2302 bp in length
4707 4806: gap of 100 bp
4807 10364: contig of 5558 bp in length
10365 10464: gap of 100 bp
10465 22143: contig of 11679 bp in length
22144 22243: gap of 100 bp
22244 31783: contig of 9540 bp in length
31784 31883: gap of 100 bp
31884 48919: contig of 17036 bp in length
48920 49019: gap of 100 bp
49020 99371: contig of 50352 bp in length
99372 99471: gap of 100 bp
99472 182383: contig of 82912 bp in length.

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/db_xref="taxon:9606"
/chromosome="11"
/map="11"
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/clone_lib="RPC1-11 Human Male BAC"
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vector_side:left"
648. 2304
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2405. 4706
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4807. 10364
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10465. 22143
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22244. 31783
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vector_side:right"
31884. 48919
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49020. 99371
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BASE COUNT 57413 a 33396 c 34191 g 56579 t 804 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60
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Db 86197 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 86138
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QY 61 GCCCTCGACC 71
|||||
Db 86137 GCCCTCGACC 86127

RESULT 10
AX280923

LOCUS AX280923 1182 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 546 from Patent WO0177172.
ACCESSION AX280923
VERSION AX280923.1 GI:16608217
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.
TITLE 1 (sites)
JOURNAL Non-endogenous, constitutively activated known g protein-coupled receptors
Patent: WO 0177172-A 546 18-OCT-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
source
1. 1182
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 292 a 343 c 241 g 306 t
ORIGIN

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Best Local Similarity 98.6%; Pred. No. 5.4e-10;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60
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Db 116 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 175
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QY 61 GCCCTCGACC 71
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Db 176 GCCCTCGACC 186

RESULT 11
AX280921
LOCUS AX280921 1203 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 544 from Patent WO0177172.
ACCESSION AX280921
VERSION AX280921.1 GI:16608216
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.
TITLE 1 (sites)
JOURNAL Non-endogenous, constitutively activated known g protein-coupled receptors
Patent: WO 0177172-A 544 18-OCT-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
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BASE COUNT 301 a 348 c 245 g 309 t
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Query Match 97.7%; Score 69.4; DB 6; Length 1203;
Best Local Similarity 98.6%; Pred. No. 5.4e-10;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 60
|||||
Db 116 GCAACCTGTCGAGCCATGCGGTCCGAACGACGACCTGGCGGAGAGACAGCCTGT 175
|||||
QY 61 GCCCTCGACC 71
|||||
Db 176 GCCCTCGACC 186

RESULT 12

AR162044
LOCUS AR162044 2160 bp DNA Linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6258556.
ACCESSION AR162044
VERSION AR162044.1 GI:16229099
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2160)
Unlabeled.
AUTHORS Unlabeled, Johnson, P., Persico, A.M. and Wang, J. Bel.
TITLE cDNA and genomic clones encoding human mu opiate receptor and the purified gene product
JOURNAL Patent: US 6258556-A 1 10-JUL-2001;
FEATURES
Location/Qualifiers
Source 1..2160
BASE COUNT 563 a 566 c 455 g 576 t
ORIGIN
Query Match 97.7% Score 69.4; DB 6; Length 2160;
Best Local Similarity 98.6%; Pred. No. 4.9e-10;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 60
DB 328 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 387
OY 61 GCCCTCGACG 71
DB 388 GCCCTCGACG 398
RESULT 13
LOCUS A87781 2162 bp DNA Linear PAT 22-JAN-2000
DEFINITION Sequence 7 from Patent WO9833937.
ACCESSION A87781
VERSION A87781.1 GI:6736383
KEYWORDS
SOURCE
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 2162)
unclassified.
AUTHORS Hoehe, M. and Wendel, B.
TITLE GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE VARIANTS, POLYMORPHISMS AND MUTATIONS THEREOF
JOURNAL Patent: WO 9833937-A 7 06-AUG-1998;
HOEHE MARGRET (DE); WENDEL BIRGIT (DE)
FEATURES
Location/Qualifiers
Source 1..2162
BASE COUNT 562 a 565 c 458 g 575 t 2 others
ORIGIN
Query Match 97.7% Score 69.4; DB 6; Length 2162;
Best Local Similarity 98.6%; Pred. No. 4.9e-10;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 60
DB 328 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 387
OY 61 GCCCTCGACG 71
DB 388 GCCCTCGACG 398
RESULT 14
LOCUS HUMORIX 2162 bp mRNA Linear PRI 08-AUG-1994
DEFINITION Human mu opiate receptor (MOR1) mRNA, complete cds.

ACCESSION L25119
VERSION L25119.1 GI:452072
KEYWORDS Mu opiate receptor.
SOURCE
ORGANISM Homo sapiens
REFERENCE
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A. and Unlabeled, R.
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 94139928
FEATURES
Location/Qualifiers
Source 1..2162
BASE COUNT 563 a 566 c 455 g 576 t 2 others
ORIGIN
Query Match 97.7% Score 69.4; DB 9; Length 2162;
Best Local Similarity 98.6%; Pred. No. 4.9e-10;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 60
DB 328 GCACCTGTCGACCGACCGGTCGACCGACCGACCGACCGACCGACCGTGT 387
OY 61 GCCCTCGACG 71
DB 388 GCCCTCGACG 398
RESULT 15
LOCUS HSU12569 1473 bp mRNA Linear PRI 12-APR-1995
DEFINITION Human mu opiate receptor variant (MOR1) mRNA, complete cds.
ACCESSION U12569
VERSION U12569.1 GI:607911
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE
AUTHORS Bare, L.A., Mansson, E. and Yang, D.
JOURNAL Expression of two variants of the human mu opiate receptor mRNA in FEBS Lett. 354 (2), 213-216 (1994)
MEDLINE 95046336
REFERENCE
Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A. and Unlabeled, R.
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic

Journal	Characterization and Chromosomal Assignment
Journal	FEBS Lett. 338 (2), 217-222 (1994)
Medline	94139928
Reference	3 (bases 1 to 1473)
Authors	Bare, L.A.
Title	Direct Submission
Journal	Submitted (24-JUL-1994) Lance A. Bare, Ohmeda, PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA
Features	Location/Qualifiers
Source	1..1473
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/cell_type="neuroblastoma, SK-N-SH"
	/tissue_type="brain"
	1..1473
gene	/gene="MOR1"
	197..1375
CDS	/gene="MOR1"
	/note="variant of human mu oploid receptor, Swiss-Prot Accession Number P35372"
	/codon_start=1
	/product="mu oploid receptor variant"
	/protein_id="AAB60354.1"
	/db_xref="gi:607912"
	/translation="MDSSAAPPTNASNCTDALAYSSCPAPSPGSMVNLISHLDDLSDP CGPRATDGGDSCPTGPSMTATITMALYSIVCGVGFGEFLVMAYIVRTKKK TATYIYFNALADALATASITLPSQVNIYNGTQPEPTILKIVSIDYMMFSITPL CTMSVDRIAYCHPYKALDPRTPPNNAIIVNCWILSSAIGLPYMFATATKRGSDID CTTFSPHTWEMLEKICVFIFAFIPVLITVYGLMLIRLSVMSLGSKEKDN LRTIRNLVVAVAFIVCMTPIHVIYIKALVTIPETFOVSWHFCIALGYNSCLN PVLAFIDENKRCRCEFCIPTSSINIDONSTRIRQNTRDHPSTANTVDRTNHQRSL"
variation	314
	/gene="MOR1"
	/citation=[2]
	/replace="a"
	/product="human mu oploid receptor"
variation	347
	/gene="MOR1"
	/citation=[2]
	/replace="g"
	/product="human mu oploid receptor"
variation	379
	/gene="MOR1"
	/citation=[2]
	/replace="g"
	/product="human mu oploid receptor"
variation	817
	/gene="MOR1"
	/citation=[2]
	/replace="g"
	/product="human mu oploid receptor"
variation	895..896
	/product="human mu oploid receptor"
variation	895..896
	/gene="MOR1"
	/citation=[2]
	/replace="cg"
	/product="human mu oploid receptor"
variation	1361..1473
	/gene="MOR1"
	/note="this variant's sequence differs from hMOR1 (GenBank Accession Number L25119) for these 113 nucleotides"
	/citation=[2]
BASE COUNT	363 a 415 c 326 g 369 t
ORIGIN	
Query Match	95.5%: Score 67.8; DB 9; Length 1473;
Best Local Similarity	97.2%: Pred. No. 1.5e-09;
Matches 69: Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
1 GCACCTGTCGACCAATGCGATCGACCGCACCGACTGGCGGGAGAGACAGCCGT 60	
312 GCGACTGTCGACCAATGCGATCGACCGCACCGACTGGCGGGAGAGACAGCCGT 371	

OY	61	GCCCTCGCACC	71
Dn	372	GCCCTCGCACC	382
<hr/>			
RESULT 16			
LOCUS	PtGMOOPR	1881 bp	MAM 03-MAR-1999
DEFINITION	Sus scrofa mu opioid receptor mRNA, complete cds.		
ACCESSION	L38645		
VERSION	L38645.1	GI:2072391	
KEYWORDS	.		
SOURCE			
ORGANISM	Sus scrofa		
	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
REFERENCE	1 (bases 1 to 1881)		
AUTHORS	Pampusch,M.S., Osinski,M.A., Brown,D.R. and Murttaugh,M.P.		
TITLE	The porcine mu opioid receptor: molecular cloning and mRNA distribution in lymphoid tissues		
JOURNAL	J. Neuroimmunol. 90 (2), 192-198 (1998)		
MEDLINE	99032385		
REFERENCE	2 (bases 1 to 1881)		
AUTHORS	Osinski,M.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology, University of Minnesota, St. Paul, MN 55108, USA On May 6, 1997 this sequence version replaced gi:1553056. Location/Qualifiers		
COMMENT FEATURES	source		
	1..1881	/organism="Sus scrofa"	
		/db_xref="taxon:9823"	
		/clone="ld7"	
		/tissue_type="cerebral cortex"	
		/note="PCR amplified"	
		237..1442	
CDS		/codon_start=1	
		/product="mu opioid receptor"	
		/protein_id="AAB53770.1"	
		/db_xref="GI:1553057"	
		/translation="MDSSADPRNANSCTDFFSPSSMCSPVPSPPSVMNFSLHGNLSLSDPCINRTIELGGSDLCPTGPSMTWTFITIMALYSIVCYVGFGENFLMYVIYVTMKTATNIYFNIALDALATALSTLPQSNNTIIMGWTPELTICKIYSISDYNNMFISFTLCTWSVDRIYAACHFPAVALDRFPTRPNKIIIVNCMIILSSAIGLFVMMAYTKIRNGSITDCALTFSHPTWYMENELIKICVFIFAIFMPVLIIIVCGMLIRLSVRLSGSKEXCDRLNRITFRMVLVVVAVETVCWTPPIHIYVIAITALITIPETFQTGSWHFCIALGYNSCLNPVIYAFIDENFKRCRFRECIPTSSTIEOONSARIIPONTRDHPSTANTVDTRNHQLENLLENFAETAAPL"	
BASE COUNT	463 a 533 c 423 g 462 t		
ORIGIN			
	Query Match	88.7%; Score 63; DB 4; Length 1881;	
	Best Local Similarity	93.0%; Pred. No. 3,3e+08;	
	Matches	66; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY	1	GCAACTGTTCGCACCATAGTGGTGCGAACGCCACGACCTGAGCGGAGAGAACAACCTGT	60
Dn	355	GCAACTGTTCGCACCATGATCGGAACCGCACGACGCTGGCGGAGAGACACCTGT	414
OY	61	GCCCTCGCACC	71
Dn	415	GCCCTCGCACC	425
<hr/>			
RESULT 17			
LOCUS	BfU08677	1415 bp	MAM 11-JAN-2000
DEFINITION	Bos taurus mu opioid receptor mRNA, complete cds.		
ACCESSION	U08677		
VERSION	U08677.2	GI:4521325	
KEYWORDS			
SOURCE	Bos taurus		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 1415)
Simon, E.J.
Onopriashvili, I., Andria, M.L., Viliim, F.S., Hiller, J.M. and Hiller, J.M.

JOURNAL
MEDLINE
20050861

REFERENCE
2 (bases 1 to 1415)
Simon, E.J., Viliim, S., Andria, M., Onopriashvili, I. and Hiller, J.M.
Direct Submission
Submitted (13-FEB-1997) Psychiatry, NYU Med. Center, 550 First Ave., New York, NY 10016, USA

REFERENCE
3 (bases 1 to 1415)
Simon, E.J., Viliim, S., Andria, M., Onopriashvili, I. and Hiller, J.M.
Direct Submission
Submitted (26-MAR-1999) Psychiatry, NYU Med. Center, 550 First Ave., New York, NY 10016, USA

REMARK
COMMENT
Sequence update by submitter
On Mar 26, 1999 this sequence version replaced gi:1881730.

FEATURES
source
location/Qualifiers
1..1415
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue.type="striatum"
156..1361
/note="G-protein coupled receptor"
/codon_start=1
/product="mu opioid receptor"
/protein_id="AAB49477.2"
/db_xref="GI:4521326"
/translation="MDSAGVPTNASCNTDPTTHSPSCSPAPSPSSWVNFHLEGLMSD
PCGPMTKLGSDRLCPSPGSPSMITAIITLALYSIVCVGLFENFLVMYIVRTKM
KTATVIFNLADALATSTLPPOSVNYLMGTPFGNLLKIVISIDYNNFTSIFT
LCTMSVDRIYAVCHPKALDLRTPRNAKIVNCWMLISSAIGLVPMFATTKYRGSIDCT
LTFSPHTWYMWENLTKICVFIFAPFIMPVLIITVCGMLIRLKSVMLSGSKREKRL
NLRITRMVLVVAVFYICWPTPHIYITKALITIPETTOTVSMHRCIALGYNSCLN
NPVLAFIDENFKRFRCFIPSTISSTIEONSIRIRONTROHPSTANTVDRTHOLEN
LEAETPLP"

CDS

BASE COUNT 337 a 430 c 309 g 339 t

ORIGIN

Query Match 86.5%; Score 61.4; DB 4; Length 1415;
Best Local Similarity 91.5%; Pred. No. 9.7e-08;
Matches 65; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGCTCCGACCGACGACCTGGCGGAGACAGACCTGT 60
|||||
DB 274 GCAACCTGTCGACCATCGCTCCGACCGACGACCTGGCGGAGACGACGACTGT 333
|||||

QY 61 GCCCTCCGACC 71
|||||

DB 334 GCCCTCCGACC 344

RESULT 18
AF074973 1334 bp mRNA linear ROD 31-AUG-1999
LOCUS
DEFINITION Mus musculus mu opioid receptor MOR1D mRNA, alternatively spliced,
complete cds.
AF074973
ACCESSION
VERSION AF074973.1 GI:5805152
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1334)
Pan, Y.-X., Xu, J., Bolan, E., Abbadie, C., Chang, A., Zuckerman, A.,
Rossi, G. and Pasternak, G.W.
Identification and characterization of three new alternatively

spliced mu-opioid receptor isoforms
Mol. Pharmacol. 56 (2), 396-403 (1999)

JOURNAL
MEDLINE
99348417

REFERENCE
PUBMED
10419560

2 (bases 1 to 1334)
Pan, Y.-X., Xu, J., Man, B.-L., Zuckerman, A.B., Rossi, G.C.,
Leventhal, L. and Pasternak, G.W.

JOURNAL
MEDLINE
Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA

FEATURES
source
location/Qualifiers
1..1334
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
67..1248
/note="alternatively spliced exon 4"
/codon_start=1
/product="mu opioid receptor MOR1D"
/protein_id="AAD51861.1"
/db_xref="GI:5805153"
/translation="MDSAGCGNISDCSDPLAPASCPAPSPSSWVNFHLEGLMSD
PNKRGLGSHSLCPQTSPPSWTAITLALYSIVCVGLFENFLVMYIVRTKMKA
TNIYIFNLADALATSTLPPOSVNYLMGTPFGNLLKIVISIDYNNFTSIFTCT
MSVDRIYAVCHPKALDLRTPRNAKIVNCWMLISSAIGLVPMFATTKYRGSIDCT
LTFSPHTWYMWENLTKICVFIFAPFIMPVLIITVCGMLIRLKSVMLSGSKREKRL
RITRMVLVVAVFYICWPTPHIYITKALITIPETTOTVSMHRCIALGYNSCLN
NPVLAFIDENFKRFRCFIPSTISSTIEONSIRIRONTROHPSTANTVDRTHOLEN
LEAETPLP"

CDS

BASE COUNT 320 a 397 c 297 g 320 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1334;
Best Local Similarity 87.3%; Pred. No. 2.3e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGCTCCGACCGACGACCTGGCGGAGACAGACCTGT 60
|||||
DB 176 GCAACCATGTCGACCATCGCTCCGACCGACGACCTGGCGGAGACGACGACTGT 235
|||||

QY 61 GCCCTCCGACC 71
|||||

DB 236 GCCCTCCGACC 246

RESULT 19
AF167566 1346 bp mRNA linear ROD 01-JAN-2002
AF167566
LOCUS
DEFINITION Mus musculus mu opioid receptor variant BI mRNA, complete cds.
AF167566
ACCESSION
VERSION AF167566.1 GI:18026692
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1346)
Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.
Identification and characterization of a mu-opioid receptor splice
variant (MOR-1B1)
Unpublished

JOURNAL
MEDLINE
2 (bases 1 to 1346)
Pan, Y.-X., Xu, J., Chang, A. and Pasternak, G.W.
Direct Submission
Submitted (12-JUL-1999) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave., New York, NY 10021, USA

FEATURES
source
location/Qualifiers
1..1346
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/chromosome="10"
/map="10A2"

RATMOP10ID 1401 bp mRNA linear ROD 24-JAN-1994
LOCUS RATMOP10ID 1401 bp mRNA linear ROD 24-JAN-1994
DEFINITION Rat mu opioid receptor mRNA, complete cds.
ACCESSION L22455
VERSION L22455.1 GI:437671
KEYWORDS mu opioid receptor.
SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1401)
REFERENCE Thompson,R.C., Mansour,A., Akil,H. and Watson,S.J.
AUTHORS Cloning and pharmacological characterization of a rat mu opioid
TITLE receptor
JOURNAL Neuron 11 (5), 903-913 (1993)
MEDLINE 94039360
FEATURES
source location/Qualifiers
1..1401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/tissue_type="olfactory bulb"
/tissue_lib="lambda ZAPil from Stratagene"
170..1366
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
/db_xref="GI:437672"
translation="MDSSTGPGNTSDCSPLAASCSPAPGSMLNLSHVNDGSDPCG
LNRIGGSDSLCPOTGSPSWYATITMALYSIVCVGLFNGFLVMYIVYTRTKRKA
TNIVFENLADALATSTLPROSVNYLNGTPEFTILCKIVISIDYVMFSTIFLCT
MSVDRTYAVCHPVKALDRTPRNAKIVAVCMWIISSAIGLPEMATTTRYOGSIDCT
LTFSPHTVWENLKIYVFIFAFIMPVLIITVCGMLRLKSVMLSGSEKDNLR
RITRMVLVVAIVFIVCMPIHIVYIKALITIPETFOVSWHFCIALGYNSCLNPV
LYAFIDENFKRCREFCIPSTSTIEQONSARIQWTRREHPSANTVDRTHQPLENLEA
ETAPLP"

BASE COUNT 330 a 434 c 312 g 325 t
ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1401;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCGACGACGACCTGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 279 GCAACGAGTCGATCGATCGCTGCAACCGACGCGGCTGCGGAGACAGCCTGT 338
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCCCTCCGACG 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 339 GCCCTCAGACC 349

RESULT 23 1423 bp mRNA linear ROD 10-SEP-1999
AF062753
LOCUS AF062753 1423 bp mRNA linear ROD 10-SEP-1999
DEFINITION Mus musculus mu opioid receptor variant C mRNA, complete cds.
ACCESSION AF062753
VERSION AF062753.1 GI:5853308
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1423)
REFERENCE Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A.,
AUTHORS Rossi,G. and Pasternak,G.W.
TITLE Identification and characterization of three new alternatively
JOURNAL spliced mu-opioid receptor isoforms
MEDLINE Mol. Pharmacol. 56 (2), 396-403 (1999)
PUBMED 99348417
10419560

REFERENCE 2 (bases 1 to 1423)
AUTHORS Pan,Y.-X., Xu,J., Wan,B.-L., Zuckerman,A.B. and Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1998) Department of Neurology, Memorial
Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021,
USA
FEATURES
source location/Qualifiers
1..1423
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
67..1383
/note="exon 4 splice variant; MOR-1C"
/codon_start=1
/product="mu opioid receptor variant C"
/protein_id="ABD34415.1"
/db_xref="GI:5853309"
translation="MDSAGPGNISDCSDPLAPASCSPAPGSMLNLSHVNDGSDPCG
PNRTGLGSHSLCPOTGSPSWYATITMALYSIVCVGLFNGFLVMYIVYTRTKRKA
TNIVFENLADALATSTLPROSVNYLNGTPEFTILCKIVISIDYVMFSTIFLCT
MSVDRTYAVCHPVKALDRTPRNAKIVAVCMWIISSAIGLPEMATTTRYOGSIDCT
LTFSPHTVWENLKIYVFIFAFIMPVLIITVCGMLRLKSVMLSGSEKDNLR
RITRMVLVVAIVFIVCMPIHIVYIKALITIPETFOVSWHFCIALGYNSCLNPV
LYAFIDENFKRCREFCIPSTSTIEQONSARIQWTRREHPSANTVDRTHQPLENLEA
VAAQIFGVPSPTHYEKPCKSCMDRGMRLNLDGDPDQESGEGQLGR"

BASE COUNT 343 a 423 c 317 g 340 t
ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1423;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCGACGACGACCTGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 176 GCAACGAGTCGACCATCGGTCGACGACGCGGCTGCGGAGACAGCCTGT 235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCCCTCCGACG 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 236 GCCCTCAGACC 246

RESULT 24 1440 bp mRNA linear ROD 22-NOV-2001
AF260306
LOCUS AF260306 1440 bp mRNA linear ROD 22-NOV-2001
DEFINITION Mus musculus mu opioid receptor isoform MOR-1Ia mRNA, complete cds,
alternatively spliced.
ACCESSION AF260306
VERSION AF260306.1 GI:17046162
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1440)
REFERENCE Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.
AUTHORS Generation of the mu opioid receptor (MOR-1) protein by three new
TITLE splice variants of the Opm gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
MEDLINE 11717463
PUBMED 11717463
REFERENCE 2 (bases 1 to 1440)
AUTHORS Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and
Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2000) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
FEATURES
source location/Qualifiers
1..1440
/organism="Mus musculus"
/strain="CXBK"
/db_xref="taxon:10090"
/chromosome="10"
/map="10A2"
<1..98
exon

CDS
19..273
/note="alternatively spliced; additional translation of this mRNA sequence deposited in Genbank Accession Number AF400246"
/codon_start=1
/product="mu oploid receptor isoform MOR-1ha"
/evidence="experimental"
/protein_id="AAL34395.1"
/db_xref="GI:17046163"
/translation="MMEAFSAFQKLRDQNOEGSYLRACPCKKLTFRRAVNGR
GGMAMPNTLECSQLOPTEASASIQNHGQRRERHRL"
99..513
/note="alternatively spliced within exon 1"
/number=1
514..866
/number=2
867..1387
/number=3
1389..>1440
/number=4
BASE COUNT 349 a 424 c 326 g 341 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 1440;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCACCTGTCCGACCCATGGTCCGAACCGACGACCTGGGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 339 GCACCGATCGACCCATGGCTCTTAACCGACGAGGGCTTGGGGAGCACAGCCTGT 398
QY 61 GCCCTCCGACC 71
||||| |||||
Db 399 GCCCTCAGACC 409
RESULT 25
AF400246 1440 bp mRNA linear ROD 22-NOV-2001
LOCUS Mus musculus mu oploid receptor 1 MOR-1 mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF400246 GI:17046392
VERSION AF400246.1
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 1440)
Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.
TITLE Generation of the mu oploid receptor (MOR-1) protein by three new
splice variants of the Opm gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
PUBMED 11717463
2 (bases 1 to 1440)
Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and
Pasternak,G.W.
REFERENCE Direct Submission
TITLE Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
JOURNAL Location/Qualifiers
FEATURES
source 1..1440
/organism="Mus musculus"
/strain="CXBK"
/db_xref="taxon:10090"
/chromosome="10"
/map="10a2"
<1..98
/number=1
99..513
/note="alternatively spliced within exon 1"
/number=1

CDS
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/codon_start=1
/product="mu oploid receptor 1 MOR-1"
/protein_id="AAL34507.1"
/db_xref="GI:17046393"
/translation="MDSAGPGNISDCSDPLAPASCPAPGSWNLNHYDGNQSDPCG
PNRTGGSGSLCPQSPSPMTATIMALYSTVCVGLGFLNLYVIVRYKMTA
TNIVYINLALADLALSTLPROSVNTLKGTPNGNLCKIVTSIDYNNETSTFCT
MSYDRITAVCHPVKALDFRPNRAKIVNCMLSSAIGLPVRFATYTRQSDICT
LTFSHPTWYENLKI CVFIFAPIMVLIITVCGMLILKSVRLSSKEDRLR
RITRVLVVAIVVAVICMTPIHIVITKALITIPETFGVSMHFCIALGYNSCLMPV
LYAFIDENFRCFRFPICPTSTTIEQONSARILQNTREHPTANTVDRTNHOLENLEA
ETAPLP"
514..866
/number=2
867..1387
/number=3
1389..>1440
/number=4
BASE COUNT 349 a 424 c 326 g 341 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 1440;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCACCTGTCCGACCCATGGTCCGAACCGACGACCTGGGGGAGAGACAGCCTGT 60
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Db 339 GCACCGATCGACCCATGGCTCTTAACCGACGAGGGCTTGGGGAGCACAGCCTGT 398
QY 61 GCCCTCCGACC 71
||||| |||||
Db 399 GCCCTCAGACC 409
RESULT 26
RNU02083 1448 bp mRNA linear ROD 20-JUL-1995
LOCUS Rattus norvegicus mu-opioid receptor mRNA, complete cds.
DEFINITION Rattus norvegicus mu-opioid receptor mRNA, complete cds.
ACCESSION U02083
VERSION U02083.1 GI:403573
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
AUTHORS 1 (bases 1 to 1448)
Bunzow,J.R., Zhang,G., Bouvier,C., Saez,C., Ronnekleiv,O.K.,
Kelly,M.J. and Grandy,D.K.
TITLE Characterization and distribution of a cloned rat mu-opioid
receptor
JOURNAL J. Neurochem. 64 (1), 14-24 (1995)
MEDLINE 95096825
2 (bases 1 to 1448)
Bunzow,J.R.
REFERENCE Direct Submission
TITLE Submitted (24-SEP-1993) James R. Bunzow, VIABR, Oregon Health
Sciences University, 3181 S.W. Sam Jackson Park Rd., Portland, OR
97201 USA
JOURNAL Location/Qualifiers
FEATURES
source 1..1448
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
/map="10116"
211..1407
/codon_start=1
/product="mu-opioid receptor"
/protein_id="AAA70049.1"
/db_xref="GI:403574"


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LNRIGLGNDSLCPTQSGSPSWYATITMALYSIVGVFEGNEFLWYIVRTKKTA
TNIYFENIALDALATSLPLROSVATYLMGTPEFGILICKIVISIDYNNFISIFPLCT
MSVDRIYAVCHRVKALDRTPRNKATIVVNCNLTSSAIGLPPMFATTKYRGSDICT
LTFSHPTVWENLKICVIFAFIMPLITIVICGLMLRLKSVMLSGSKRDNLR
RITRNLVAVVAVFICWTPHIVYIKALITIPETFOVSWHFCIALGYTSCNLP
LYAFIDENFKRCFREFCIPSTSTIEQONSFRVONTREHPSANTVDRTNHOLENLEA
ETAPLP"
BASE COUNT      345 a      443 c      326 g      334 t
ORIGIN

Query Match      79.7%; Score 56.6; DB 10; Length 1448;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGCCAGCCATCGGTCCGACCGACGACCTGGCGGGAGAGACGCTGT 60
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DB 320 GCACACGATCGCATCGGTGACCGCGCTTGCGGGAAACGACGCTGT 379
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCCCTCGGACG 71
      ||||| |||||
DB 380 GCCCTGAGACG 390

RESULT 27      1543 bp mRNA linear ROD 31-AUG-1999
AF074974
LOCUS      Mus musculus mu opioid receptor MOR1e mRNA, alternatively spliced,
DEFINITION complete cds.
ACCESSION      AF074974
VERSION      AF074974.1 GI:5805154
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 1543)
AUTHORS      Pan,Y.X., Xu,J., Bolan,E., Abdadie,C., Chang,A., Zuckerman,A.,
Rossi,G., and Pasternak,G.W.
TITLE      Identification and characterization of three new alternatively
spliced mu-opioid receptor isoforms
JOURNAL      Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE      99348417
PUBMED      10419560
CDS      2 (bases 1 to 1543)
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            /number=1
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            /product="mu opioid receptor MOR1e"
            /protein_id="A051862.1"
            /db_xref="GI:5805155"
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            PNRTIGGSHSLCPQSGSPSWYATITMALYSIVGVFEGNEFLWYIVRTKKTA
            TNIYFENIALDALATSLPLROSVATYLMGTPEFGILICKIVISIDYNNFISIFPLCT
            MSVDRIYAVCHRVKALDRTPRNKATIVVNCNLTSSAIGLPPMFATTKYRGSDICT
            LTFSHPTVWENLKICVIFAFIMPLITIVICGLMLRLKSVMLSGSKRDNLR
            RITRNLVAVVAVFICWTPHIVYIKALITIPETFOVSWHFCIALGYTSCNLP
            LYAFIDENFKRCFREFCIPSTSTIEQONSFRVONTREHPSANTVDRTNHOKKLLDS
            ORGVQHHV"
BASE COUNT      369 a      455 c      345 g      374 t
ORIGIN

Query Match      79.7%; Score 56.6; DB 10; Length 1543;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGCCAGCCATCGGTCCGACCGACGACCTGGCGGGAGAGACGCTGT 60
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DB 176 GCACACGATCGCATCGGTGACCGCGCTTGCGGGAAACGACGCTGT 235
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QY 61 GCCCTCGGACG 71
      ||||| |||||
DB 236 GCCCTGAGACG 246

RESULT 28      1569 bp mRNA linear ROD 22-NOV-2001
AF260308
LOCUS      Mus musculus mu opioid receptor isoform MOR-1Ja mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION      AF260308
VERSION      AF260308.1 GI:17046166
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 1569)
AUTHORS      Pan,Y.X., Xu,J., Mahutier,L., Bolan,E., Xu,M., and Pasternak,G.W.
TITLE      Generation of the mu opioid receptor (MOR-1) protein by three new
splice variants of the Oprm gene
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
PUBMED      11717463
REFERENCE      2 (bases 1 to 1569)
AUTHORS      Pan,Y.X., Xu,J., Rossi,G., Xu,M., Mahutier,L., Bolan,E. and
Pasternak,G.W.
TITLE      Direct Submission
JOURNAL      Submitted (25-Apr-2000) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
FEATURES
SOURCE      1..1569
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ORIGIN

Query Match      79.7%; Score 56.6; DB 10; Length 1569;
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Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 468 GCAACCACTCGACCGATCGGCTCTTAACCGACGAGGGGCTTGGCGGAGCAGACGCTGT 527
Qy 61 GCCCTCCGACC 71
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Db 528 GCCCTCAGACC 538

RESULT 29
AF400248 1569 bp mRNA linear ROD 22-NOV-2001
LOCUS Mus musculus mu opioid receptor 1 mRNA, complete cds, alternatively
DEFINITION spliced.
ACCESSION AF400248
VERSION AF400248.1 GI:17046396
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 1569)
Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.
Generation of the mu opioid receptor (MOR-1) protein by three new
JOURNAL splice variants of the Oprm gene
PUBMED Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
11717463
2 (bases 1 to 1569)
Pan,Y.X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and
PASTERNAK,G.W.
Direct Submission
TITLE Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer
JOURNAL Center, 1275 York Ave, New York, NY 10021, USA
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source
1. 1569
Location/Qualifiers
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/strain="CXBK"
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99. 227
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228. 642
exon
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359. 1555
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this mRNA sequence deposited in Genbank Accession Number
AF60308"
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/db_xref="GI:17046397"
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MSVDRIYAVCHPYKALDFRTPRNKATVNCNWLSSAIGLPVPMATTKYRQSIDCT
LTSHPFTWENLTKICVLFAPIMPLIITIVCYGLMLKSVRMLSGSKEDRNLR
RITRMVLVVAIVAVICWTPPIHIVIIKALITITPETFGVSMHFCIALYNSCLNLP
LVAFDENFRCFRRCFIPSTSTIEQONSARIRQNTREHSTANTVDRTHOLENLEA
ETAPLP"

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exon 996. 1516
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exon 1517. 1569
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ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1569;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAACCTGTCGACCGATCGGCTCTTAACCGACGAGGGGCTTGGCGGAGAGACGCTGT 60

Db 468 GCAACCACTCGACCGATCGGCTCTTAACCGACGAGGGGCTTGGCGGAGCAGACGCTGT 527
Qy 61 GCCCTCCGACC 71
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Db 528 GCCCTCAGACC 538

RESULT 30
RATMORA 1586 bp mRNA linear ROD 04-AUG-1993
LOCUS Rattus norvegicus mu opioid receptor mRNA, complete cds.
DEFINITION R13069
ACCESSION I13069
VERSION I13069.1 GI:348250
KEYWORDS mu opioid receptor.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus Whole brain cDNA to mRNA.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
TITLE 1 (bases 1 to 1586)
Chen,Y., Mestek,A., Liu,J., Hurley,J.A. and Yu,L.
Molecular cloning and functional expression of a mu-opioid receptor
JOURNAL from rat brain
MEDLINE Mol. Pharmacol. 44, 8-12 (1993)
93341493
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1. 1586
Location/Qualifiers
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210. 1406
/codon_start=1
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MSVDRIYAVCHPYKALDFRTPRNKATVNCNWLSSAIGLPVPMATTKYRQSIDCT
LTSHPFTWENLTKICVLFAPIMPLIITIVCYGLMLKSVRMLSGSKEDRNLR
RITRMVLVVAIVAVICWTPPIHIVIIKALITITPETFGVSMHFCIALYNSCLNLP
LVAFDENFRCFRRCFIPSTSTIEQONSARIRQNTREHSTANTVDRTHOLENLEA
ETAPLP"

BASE COUNT 376 a 479 c 361 g 370 t
ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 1586;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAACCTGTCGACCGATCGGCTCTTAACCGACGAGGGGCTTGGCGGAGAGACGCTGT 60
Db 319 GCAACCACTCGACCGATCGGCTCTTAACCGACGAGGGGCTTGGCGGAGAGACGCTGT 378

Qy 61 GCCCTCCGACC 71
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Db 379 GCCCTCAGACC 389

RESULT 31
MMU26915 1610 bp mRNA linear ROD 09-NOV-1995
LOCUS Mus musculus mu opioid receptor (MOR-1) mRNA, complete cds.
ACCESSION U26915
VERSION U26915.1 GI:1055230
KEYWORDS house mouse.
SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1610)
AUTHORS Rossi,G.C., Pan,Y.X., Brown,G.P. and Pasternak,G.W.
TITLE Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide receptor
JOURNAL FEBS Lett. 369 (2-3), 192-196 (1995)
MEDLINE 95377399
REFERENCE 2 (bases 1 to 1610)
AUTHORS Pan,Y.-X.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1995) Ying-Xian Pan, Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

FEATURES
source location/Qualifiers
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/db_xref="taxon:10090"
/tissue_type="brain"
1..1610
/gene="MOR-1"
283..1479
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/protein_id="AA81170.1"
/db_xref="GI:1055231"
/translation="MDSASRGNISDCSDPLAPASCSPAPGSM.LSHVQNSDPG
FNRTLGSGSHSLCPQTGSPSMYATITMALVSVVGLFGLVWYIVRTKKTA
TNIYFENLADALATSTLPQSVNKLMTWFGNLTGKIVISIDYNNFTSIFLCT
MSVDRYIAVCHKALDERTPENAKIVNVCMI LSSAIGLPYPMATTKYRGSIDCT
LTFSHPTWMEWLKICVEIFAFIMPELITIVCYGLMLRLKRSVMSLGSKRDNLR
RTIRNVLVVAIVFICWTPITPHIVYIKALITIPETPTQSVSHFPLATCYTSCINPV
LYARIDENFKRCFRFCIPTSSTIEQNSARIRONTREHPSTANTVDRTNHOLENLEA
ETAPLP"

BASE COUNT 373 a 476 c 368 g 393 t
ORIGIN

Query Match 79.7% Score 56.6; DB 10; Length 1610;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 392 GCAACGAGTCGACCCATGGTCCGACCGACCGACCGGCGGTGGCGGAGCACAGCCTGT 451
QY 61 GCCCTCCGAC 71
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Db 452 GCCCTCAGAC 462

RESULT 32
AF260307 1614 bp mRNA linear ROD 22-NOV-2001
LOCUS Mus musculus mu opioid receptor isoform MOR-11a mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF260307
VERSION AF260307.1 GI:17046164
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
MEDLINE 11717463
REFERENCE 2 (bases 1 to 1614)
AUTHORS Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and
Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2000) Neurology, Memorial Sloan-Kettering Cancer

Center, 1275 York Ave, New York, NY 10021, USA

FEATURES
source location/Qualifiers
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this mRNA sequence deposited in Genbank Accession Number
AF400247"
/codon_start=1
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/protein_id="AAL34396.1"
/db_xref="GI:17046165"
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LMGC"
99..687
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688..1040
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1041..1561
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1562..>1614
/number=4

BASE COUNT 381 a 477 c 373 g 383 t
ORIGIN

Query Match 79.7% Score 56.6; DB 10; Length 1614;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGGTCCGACCGACCGACCTGGCGGAGACAGCCTGT 60
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Db 513 GCAACGAGTCGACCCATGGTCCGACCGACCGGCGGTGGCGGAGCACAGCCTGT 572
QY 61 GCCCTCCGAC 71
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Db 573 GCCCTCAGAC 583

RESULT 33
AF400247 1614 bp mRNA linear ROD 22-NOV-2001
LOCUS Mus musculus mu opioid receptor 1 MOR-1 mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF400247
VERSION AF400247.1 GI:17046194
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Pan,Y.X., Xu,J., Mahurter,L., Bolan,E., Xu,M. and Pasternak,G.W.
TITLE Generation of the mu opioid receptor (MOR-1) protein by three new
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (24), 14084-14089 (2001)
MEDLINE 11717463
REFERENCE 2 (bases 1 to 1614)
AUTHORS Pan,Y.-X., Xu,J., Rossi,G., Xu,M., Mahurter,L., Bolan,E. and
Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-2001) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA

FEATURES
source location/Qualifiers
1..1614
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/strain="CXBK"
/db_xref="taxon:10090"
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exon /number=11
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404..1600
/note="alternatively spliced; additional translation of
this mRNA sequence deposited in GenBank Accession Number
AF260307"
/codon_start=1
/product="mu opioid receptor 1 MOR-1"
/db_xref="GI:17046395"
/translation="MDSSAGPNIISDCSDPLADASCSPADGSMILNSHVDGNSDPG
PNRTGLGSHSLCPOTGSPSMVTATITMALYSIVCVGLNLYVYVIRYKMTA
TNIYFINLADALATSTLPQSVNLTGMPGNLICKIVISIDYNNMPTSIETCT
MSYDRYAVCHPVALDEPRNAKIVNCGNMLSSAGLPMVEMATKXROSDICT
LFRSHPTWYENLKICVFTEAFRIALITTCVGLMILKSVRLSGSKEDNR
RITRMVLVVAIVTICVTPTHIYVITKALITTEPTQTSMHFCIALGTNSCLNP
LYAFDENFRCFRECIPTSTIEQNSARIKONTREHPSTANTYDRTWOLENLEA
ETAPLP"
exon 688..1040
/number=2
1041..1561
/number=3
1562..>1614
/number=4
BASE COUNT 381 a 477 c 373 g 383 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 1614;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACGACCTGGCGGGAGAGACAGCCTGT 60
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Db 513 GCAACCACTCCGACCCATGCGGTCTTAACCGACGAGGGCTTGGCGGAGCCACAGCCTGT 572
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 GCCCTCGACG 71
||||| |||||
Db 573 GCCCTCAGACG 583
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
RESULT 34
LOCUS AR106013 1618 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6103492.
ACCESSION AR106013
VERSION AR106013.1 GI:12820078
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1618)
AUTHORS Yu, L.
TITLE Polynucleotide encoding mu opioid receptor
JOURNAL Patent: US 6103492-A 15-AUG-2000;
FEATURES
source Location/Qualifiers
1..1618
/organism="unknown"
BASE COUNT 390 a 486 c 370 g 372 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 6; Length 1618;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACGACCTGGCGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 323 GCAACCACTCCGACCCATGCGGTCTGAACCGACGAGGGCTTGGCGGAGACAGCAGCCTGT 382
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 GCCCTCGACG 71
||||| |||||
Db 383 GCCCTCAGACG 393
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 35
LOCUS AR106014 1618 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6103492.
ACCESSION AR106014
VERSION AR106014.1 GI:12820079
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1618)
AUTHORS Yu, L.
TITLE Polynucleotide encoding mu opioid receptor
JOURNAL Patent: US 6103492-A 3 15-AUG-2000;
FEATURES
source Location/Qualifiers
1..1618
/organism="unknown"
BASE COUNT 390 a 486 c 370 g 372 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 6; Length 1618;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACGACCTGGCGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 323 GCAACCACTCCGACCCATGCGGTCTGAACCGACGAGGGCTTGGCGGAGACAGCAGCCTGT 582
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 GCCCTCGACG 71
||||| |||||
Db 383 GCCCTCAGACG 393
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
RESULT 37
LOCUS AR153355 1618 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6235496.
ACCESSION AR153355
VERSION AR153355.1 GI:15120887
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACGACCTGGCGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 323 GCAACCACTCCGACCCATGCGGTCTGAACCGACGAGGGCTTGGCGGAGACAGCAGCCTGT 382
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 GCCCTCGACG 71
||||| |||||
Db 383 GCCCTCAGACG 393
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1618)
AUTHORS Yu, L.
TITLE Nucleic acid encoding mammalian mu opioid receptor
JOURNAL Patent: US 6235496-A 3 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..1618
/organism="unknown"
BASE COUNT 390 a 486 c 370 g 372 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 6; Length 1618;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCATCGGTCCGAGCCGACCTGTGGCGGAGAGACAGCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 GCAACCACTCCGATCCGATCGGTCTGAAACCGACCGCGCTTGGCGGAGACAGACCTGT 382
QY 61 GCCCTCCGACC 71
||||| |||||
DB 383 GCCCTCAGACC 393
RESULT 38
AF167568 1729 bp mRNA linear ROD 28-JUN-2000
LOCUS AF167568
DEFINITION Mus musculus mu opioid receptor variant F mRNA, complete cds.
ACCESSION AF167568
VERSION AF167568.1 GI:8778197
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1729)
AUTHORS Pan, Y.-X., Xu, J., Bolan, E., Chang, A., Mahurter, L., Rossi, G. and
Pasternak, G.W.
TITLE Isolation and expression of a novel alternatively spliced mu opioid
JOURNAL receptor isoform, MOR-1F
MEDLINE FEBS Lett. 466 (2-3), 337-340 (2000)
PUBMED 10682855
REFERENCE 2 (bases 1 to 1729)
AUTHORS Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2000) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave., New York, NY 10021, USA
FEATURES Location/Qualifiers
source 1..1729
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/chromosome="10"
/map="10A2"
67..1401
/note="MOR-1F; alternatively spliced variant of MOR-1
gene"
/codon_start=1
/product="mu opioid receptor variant F"
/protein_id="AA79213.1"
/db_xref="GI:8778198"
/translation="MDSSAGPNISSDCSDPLAPASCPAPGSLWNLSDVGNOSDPCG
PNTGLGSHSLCPOTGSPSPVATITIMALYSICVYGLGSLVIMVIVRYTKMTA
TNIYFNLALADALATSLPPOSVNYMTGMPENICIKIIVISIDYNNMETSIPFLCT
MSVDRIYAVGHVYKALDEPRTNRNKKIYNNCMILSSAIGPVMNMTYKROGSDICT
LIRSHPTWYNELKICVFIAPFIMPVLIITVCTGLMILRLKSVRLSGSKEDRNLR
RTIRMLVAVAVELVCFWPHIYVITIALITITPTTQTVSMHCIALGSKNSCLNPL
LYAFIDENFRCFREPCIPSTTEONSARIRONTREHPSSTANTVDRTHQACACV
PGANRGTKASDLIDLELTVGSHQADATNPGRYEGSKCAEPLAISLPLY"

BASE COUNT 417 a 505 c 395 g 412 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 1729;
Best Local Similarity 87.3%; Pred. No. 2.2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCATCGGTCCGAGCCGACCTGTGGCGGAGAGACAGCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 176 GCAACCACTCCGACCATCGGTCTTACCGACGCGGCTTGGCGGAGACAGACCTGT 235
QY 61 GCCCTCCGACC 71
||||| |||||
DB 236 GCCCTCAGACC 246
RESULT 39
S79903 1944 bp DNA linear ROD 17-FEB-1996
LOCUS S79903
DEFINITION mu opioid receptor (exon 1, promoter) [rats, Genomic, 1944 nt].
ACCESSION S79903
VERSION S79903.1 GI:1195532
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1944)
AUTHORS Kraus, J., Horn, G., Zimprich, A., Simon, T., Mayer, P. and Hollt, V.
TITLE Molecular cloning and functional analysis of the rat mu opioid
JOURNAL receptor gene promoter
MEDLINE Biochem. Biophys. Res. Commun. 215 (2), 591-597 (1995)
REMARK 96011819
GenBank staff at the National Library of Medicine created this
entry [NCBI gidsbg 172339] from the original journal article.
This sequence comes from Fig. 1.
FEATURES Location/Qualifiers
source 1..1944
/organism="Rattus sp."
/db_xref="taxon:10118"
1361..>1944
1661..1944
/partial
gene
mRNA
gene
BASE COUNT 498 a 468 c 446 g 532 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 1944;
Best Local Similarity 87.3%; Pred. No. 2.1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCATCGGTCCGAGCCGACCTGTGGCGGAGAGACAGCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1770 GCAACCACTCCGATCCGATCGGTCTGAAACCGACCGGCTTGGCGGAGACAGCTGT 1829
QY 61 GCCCTCCGACC 71
||||| |||||
DB 1830 GCCCTCAGACC 1840
RESULT 40
AF167567 2045 bp mRNA linear ROD 01-JAN-2002
LOCUS AF167567
DEFINITION Mus musculus mu opioid receptor variant B11 mRNA, complete cds.
ACCESSION AF167567
VERSION AF167567.1 GI:18026694
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2045)

AUTHORS Pan, Y.-X., Xu, J., Chang, A., Mahurter, L. and Pasternak, G.W.
TITLE Identification and characterization of a novel mu opioid receptor splice variant (MOR-1BII)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2045)
AUTHORS Pan, Y.-X., Xu, J., Chang, A. and Pasternak, G.W.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA
FEATURES
source
1. 2045
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/chromosome="10"
/map="10A2"
67..1296
/note="MOR-1BII: alternatively spliced variant of MOR-1 gene"
/codon_start=1
/product="mu opioid receptor variant BII"
/protein_id="AA15583.1"
/db_xref="GI:18026695"
/translation="MDSNAGPNTSCSPPLAPASGSPAPGSLNLSHYDGNQSDPCGPNRTGLGSHSLCPOTGSPSWATITIMALYSIVCVGLFNGFLVMYVIRTKMTATNIIYFNLAADALATSTLPQSVNTLMCTGKIVISIDYNNMTSIFLTCTMSVDRIAVCHDPAKADFPRTPNKIVNOCNMLSSAIGLIPVFNATITRYROSDICTLFESEPTWYVENLTKICVFIAPFIMPVLTIVCGMILRLKSVRLSGSKEDRNLRITRWLVVAVAVIVCMTPIHIIYIITIKITITIDETFEQVSMHFCALIGTNSCLNPLVYAFIDENFKRCRECIPTSTIIEQONSARIRQNRHNPSTANTYDRINHOXLMWRAMPFRRLHIALMLSDN"
BASE COUNT 521 a 525 c 423 g 576 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 2045;
Best local Similarity 87.3%; Pred. No. 2, 1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGGGTCCGACCGACCTGGGGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 176 GCAACCAAGTCCGACCATGGGTCTTAACCGACGGGGCTTGGGGGAGCAGACGCTGT 235
QY 61 GCCCTCGACC 71
||||| ||||||| |||
Db 236 GCCCTCAGACC 246
RESULT 41
LOCUS MMOR1 2093 bp DNA linear ROD 08-NOV-1994
DEFINITION Mus musculus mu opioid receptor (MOR) gene, exon 1.
ACCESSION U10558
VERSION U10558.1 GI:565065
KEYWORDS
SEGMENT 1 of 4
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2084)
AUTHORS Min, B.H., Augustin, L.B., Felsheim, R.F., Fuchs, J.A. and Loh, H.H.
TITLE Genomic structure analysis of promoter sequence of a mouse mu opioid receptor gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (19), 9081-9085 (1994)
MEDLINE 94377496
REFERENCE 2 (bases 1 to 2093)
AUTHORS Augustin, L.B.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-1994) Lance B. Augustin, Pharmacology, University of Minnesota, 435 Delaware Street SE, Minneapolis, MN 55455, USA
FEATURES
source
1. 2093
/organism="Mus musculus"

/strain="C57 Black/6"
/db_xref="taxon:10090"
/clone="lambdaMOR2"
/tissue_type="liver"
/clone_lib="Stratagene Number 945301"
/dev_stage="adult"
CAAT_signal 1393..1397
5'UTR 1533..1800
exon /gene="MOR"
1533..2084
/gene="MOR"
/number=1
prim_transcript 1533..>2093
/gene="MOR"
2085..>2093
intron /gene="MOR"
BASE COUNT 551 a 495 c 474 g 573 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 10; Length 2093;
Best local Similarity 87.3%; Pred. No. 2, 1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGGGTCCGACCGACCACTGGGGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1910 GCAACCAAGTCCGACCATGGGTCTTAACCGACGGGGCTTGGGGGAGCAGACGCTGT 1969
QY 61 GCCCTCGACC 71
||||| ||||||| |||
Db 1970 GCCCTCAGACC 1980
RESULT 42
LOCUS AR148257 2135 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6225080.
ACCESSION AR148257
VERSION AR148257.1 GI:15112347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2135)
AUTHORS Uhl, G.R., Eppler, C. Mark, and Wang, J.-B.
TITLE Mu-subtype opioid receptor
JOURNAL Patent: US 6225080-A 1 01-MAY-2001;
FEATURES
source
1. 2135
/organism="unknown"
BASE COUNT 541 a 590 c 441 g 563 t
ORIGIN
Query Match 79.7%; Score 56.6; DB 6; Length 2135;
Best local Similarity 87.3%; Pred. No. 2, 1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGGGTCCGACCGACCACTGGGGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 140 GCAACCAAGTCCGACCATGGGTCTTAACCGACCGGGCTTGGGGGAGAGACAGCCTGT 199
QY 61 GCCCTCGACC 71
||||| ||||||| |||
Db 200 GCCCTCAGACC 210
RESULT 43
LOCUS RATMOR1A 2135 bp mRNA linear ROD 21-OCT-1993
DEFINITION Rattus norvegicus Mu opiate receptor (MOR1) mRNA, complete cds.
ACCESSION L20684
VERSION L20684.1 GI:409149
KEYWORDS Mu opiate receptor.
SOURCE Rattus norvegicus (library: lambda ZAP (Stratagene)) cortex cDNA to

ORGANISM mRNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2135)
AUTHORS Wang, J.-B., Imai, Y., Eppler, M.C., Gregor, P., Spiwak, C. and Uhl, G.R.
TITLE Mu opiate receptor: cDNA cloning and expression
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234 (1993)
MEDLINE 94052137
FEATURES
source location/Qualifiers
1..2135
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="cortex"
/tissue_idb="lambda ZAP (Stratagene)"
1..2135
/gene="MUOR1"
31..1227
/gene="MUOR1"
/codon_start=1
/product="mu opiate receptor"
/protein_id="AAA41643.1"
/db_xref="GI:409150"
/translation="MDSSTGPGNTSDCSPLAASCPAPGSMNLISHVDGNQSDPCG
LNRGLGGNSLCPQTGSPSWATTTTALSTIVCVGLFGNPLVMYIVRTKMTA
TNIYFENLADALATSTLPQSVNYLMTGTPGNILCKIVISIDYNNMPTSTLCT
MSVDRIYAVCHPVKALDRTPRNAKIVVNCNIISSAIGLPVMEATTKYRGSDICT
LTFSPHTWYMWENLTKICVFIFAFIMPVLITIVCGYGLMLRLKSVMLSGSKERDNL
RTRRWLVVAVFIVCWPTPIHIVYIKALITIPETTPQTVSMHFCIALGYNSCLNPV
LYAFIDENFKRCFRFCIPSTSTIEQNSARI RONTREHPSTANTVDRTNHLENLEA
ETAPLP"

BASE COUNT 541 a 590 c 441 g 563 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 2135;
Best Local Similarity 87.3%; Pred. No. 2.1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCACCTGTCGCCACCATCGGTCGACGACGACGACCTGGCGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 140 GCACACGTCGCATCGCTGACGACGACGCGGCTTGCGGAGACGACGCTGT 199

OY 61 GCCCTCGCAGC 71
||||| |||||||
Db 200 GCCCTAGACC 210

RESULT 44
AB047546 2137 bp mRNA linear ROD 22-AUG-2001
LOCUS Mus musculus MOR mRNA for mu opioid receptor, complete cds.
DEFINITION AB047546
VERSION AB047546.1 GI:15277133
KEYWORDS
SOURCE Mus musculus
ORGANISM Mus musculus (strain: CXB-7/By) male brain cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2137)
AUTHORS Ikeda, K., Kobayashi, T., Ichikawa, T., Kumanishi, T., Niki, H. and
Yano, R.
TITLE The untranslated region of m-opioid-receptor mRNA contributes to
reduced opioid sensitivity in CXBR mice
J. Neurosci. (2000) In press
2 (bases 1 to 2137)
Ikeda, K.
DIRECT SUBMISSION
JOURNAL Submitted (21-AUG-2000) Kazutaka Ikeda, RIKEN Brain Science
Institute, Neurobiology of Emotion Laboratory, 2-1 Hirotsawa, Wako,
Saitama 351-0198, Japan (E-mail: ikeda@postman.riken.go.jp,
Tel: 81-48-462-1111 (ex. 6436), Fax: 81-48-467-9645)
FEATURES
Location/Qualifiers

source 1..2137
/organism="Mus musculus"
/strain="CXB-7/By"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="brain"
215..1411
/gene="MOR"
215..1411
/gene="MOR"
/codon_start=1
/product="mu opioid receptor"
/protein_id="BAB63338.1"
/db_xref="GI:15277134"
/translation="MDSAGPGNISDCSPLAPASCPAPGSMNLISHVDGNQSDPCG
PNRGLGGSHSLCPQTGSPSWATTTTALSTIVCVGLFGNPLVMYIVRTKMTA
TNIYFENLADALATSTLPQSVNYLMTGTPGNILCKIVISIDYNNMPTSTLCT
MSVDRIYAVCHPVKALDRTPRNAKIVVNCNIISSAIGLPVMEATTKYRGSDICT
LTFSPHTWYMWENLTKICVFIFAFIMPVLITIVCGYGLMLRLKSVMLSGSKERDNL
RTRRWLVVAVFIVCWPTPIHIVYIKALITIPETTPQTVSMHFCIALGYNSCLNPV
LYAFIDENFKRCFRFCIPSTSTIEQNSARI RONTREHPSTANTVDRTNHLENLEA
ETAPLP"

BASE COUNT 540 a 581 c 471 g 545 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 10; Length 2137;
Best Local Similarity 87.3%; Pred. No. 2.1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCACCTGTCGCCACCATCGGTCGACGACGACGACCTGGCGGGAGAGACAGCCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 324 GCACACGTCGCCACCATCGGTCCTAACGACGCGGCTTGCGGAGACGACGCTGT 383

OY 61 GCCCTCGCAGC 71
||||| |||||||
Db 384 GCCCTAGACC 394

RESULT 45
A68824 2229 bp DNA linear PAT 06-MAY-1999
LOCUS A68824
DEFINITION Sequence 1 from Patent WO9802534.
ACCESSION A68824
VERSION A68824.1 GI:4759752
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Kieffer, B.L., Matthes, H.W., Simonin, F.H., Dietrich, A. and Lemoine, M.
AUTHORS TITLE TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS
MODIFIED
JOURNAL Patent: WO 9802534-A 1 22-JAN-1998;
COMMENT CENTRE NAT RECH SCIENT (FR)
FEATURES Other publication FR 2750825 19980116.
source location/Qualifiers
1..2229
/organism="unidentified"
/db_xref="taxon:32644"
256..1452
/note="unnamed protein product"
/codon_start=1
/protein_id="CABA2460.1"
/db_xref="GI:4759753"
/translation="MDSAGPGNISDCSPLAPASCPAPGSMNLISHVDGNQSDPCG
PNRGLGGSHSLCPQTGSPSWATTTTALSTIVCVGLFGNPLVMYIVRTKMTA
TNIYFENLADALATSTLPQSVNYLMTGTPGNILCKIVISIDYNNMPTSTLCT
MSVDRIYAVCHPVKALDRTPRNAKIVVNCNIISSAIGLPVMEATTKYRGSDICT
LTFSPHTWYMWENLTKICVFIFAFIMPVLITIVCGYGLMLRLKSVMLSGSKERDNL
RTRRWLVVAVFIVCWPTPIHIVYIKALITIPETTPQTVSMHFCIALGYNSCLNPV
LYAFIDENFKRCFRFCIPSTSTIEQNSARI RONTREHPSTANTVDRTNHLENLEA
ETAPLP"

BASE COUNT 562 a 608 c 489 g 570 t

ORIGIN

Query Match 79.7%; Score 56.6; DB 6; Length 2229;
Best Local Similarity 87.3%; Pred. No. 2.1e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGTCCGACGACCGACCTGGGGAGAGACGCTGT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 365 GCAACGATCGACCGATCGGCTCTAACCGACGCGGCTTGGCGGAGCACAGCCTGT 424

QY 61 GCCCTCGACC 71
||||| |||||

Db 425 GCCCTCAGACC 435

RESULT 46
MMU19380 2229 bp mRNA linear ROD 07-FEB-1996

LOCUS Mus musculus mu opioid receptor cDNA, complete cds.
DEFINITION U19380
ACCESSION U19380.1 GI:885864
VERSION
KEYWORDS
SOURCE house mouse
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Kaufman, D.L., Keith, D.E., Anton, B., Tian, J., Magendzo, K.,
Nemman, D., Tran, T., Lee, D.S., Wen, C., Xia, Y., Lusis, A.J. and
Evans, C.J.
TITLE Characterization of the murine mu opioid receptor gene
JOURNAL J. Biol. Chem. 270 (26), 15877-15883 (1995)
MEDLINE 95318184
REFERENCE 2 (bases 1 to 2229)
AUTHORS Evans, C.C.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-1995) Christopher J Evans, Psychiatry and
Biobehavioral Sciences, University of California at Los Angeles,
UCLA-NPI, 760 Westwood Plaza, Los Angeles, CA 90024-1759, USA

FEATURES
source location/Qualifiers
1..2229
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="mMOR"
/tissue="brain"
/dev_stage="adult"
/note="in lambda gtl0"
256..1452
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA86878.1"
/db_xref="GI:885865"
/translation="MDSAGPGNISDCSDPLAPASMPARGSLNLSHVNGNSDPG
PNRTGLGSHSLCPGTSPSMVAITIMALYSIVCVGLGNELVYIVRYTKMTA
TNTIYFNLAALADALATSTLPQSVNLTMPGTLKIVISIDVNMETSIFLTCT
MSYDRYIAVCHPYKALDFRPRNAKIVNVCNMLSSAIGLPMFMAATTKRGSIDCT
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CDS
BASE COUNT 562 a 608 c 489 g 570 t
ORIGIN

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Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 365 GCAACGATCGACCGATCGGCTCTAACCGACGCGGCTTGGCGGAGCACAGCCTGT 424

QY 61 GCCCTCGACC 71
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Db 425 GCCCTCAGACC 435

Db 425 GCCCTCAGACC 435
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RESULT 47
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LOCUS Rat mRNA for rat opioid receptor B, complete cds.
DEFINITION D16349
ACCESSION D16349.1 GI:391866
VERSION
KEYWORDS G-protein coupled receptor; rat opioid receptors; transmembrane
protein.
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
PROR15.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Takeshima, H.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1993) Hiroshi Takeshima, International Institute
for Advanced Studies, C/O Shimadzu Corporation N-80, 1
Nishinokyo-Kuwanara-cho, Kyoto 604, Japan (tel:075-823-1208,
fax:075-811-8186)
2 (bases 1 to 2397)
Fukuda, K., Kato, S., Mori, K., Nishi, M. and Takeshima, H.
TITLE Primary structures and expression from cDNAs of rat opioid receptor
delta- and mu-subtypes
FEBS Lett. 327 (3), 311-314 (1993)
93351652
COMMENT Submitted (03-JUN-1993) to DDBJ by:
Hiroshi Takeshima
International Institute for
Advanced Studies
C/O Shimadzu Corporation N-80
1 Nishinokyo-Kuwanara-cho
Kyoto 604
Japan
Phone: 075-823-1208
Fax: 075-811-8186.

FEATURES
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LYAFIDENFKRCFREFCIPSTSTIEQNSARIKONTREHPSTANTVDRTNHOLENLEA
ETAPLP"

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BASE COUNT 614 a 650 c 506 g 627 t
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Best Local Similarity 87.3%; Pred. No. 2e-06;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 61 GCCCTCGGACC 71
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RESULT 49
AX346295/c 6494 bp DNA linear PAT 01-FEB-2002
LOCUS
DEFINITION Sequence 1366 from Patent WO0200928.
ACCESSION AX346295
VERSION AX346295.1 GI:18494181
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 1366 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
Source 1..6494
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
BASE COUNT 1929 a 81 c 1179 g 3305 t
ORIGIN

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Matches 57; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 1114 CCCCTCGGACC 1105

RESULT 50
AX348524/c 6494 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 32 from Patent WO0202809.
ACCESSION AX348524
VERSION AX348524.1 GI:18614559
KEYWORDS
SOURCE .
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of behavioural disorders, neurological disorders and
cancer
JOURNAL Patent: WO 0202809-A 32 10-JAN-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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BASE COUNT 1929 a 81 c 1179 g 3305 t
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Matches 57; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 62 CCCCTCGGACC 71
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:16:52 : Search time 206 Seconds
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Title: US-09-626-616-7_COPY_354_424

Perfect score: 71

Sequence: 1 GCAACGCTGCGACCGACATGC.....ACAGCGCTGCGCTCGACAC 71

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1737030

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
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2	71	100.0	1610	21	AA059503	cDNA encoding a hu
3	69.4	97.7	1182	23	AB198013	Non-endogenous hum
4	69.4	97.7	1203	23	AB198012	Non-endogenous hum
5	69.4	97.7	2160	16	AA093102	Human mu opiate re
6	69.4	97.7	2162	19	AAV61985	Human mu-opioid re
7	69.4	97.7	2162	19	AAV61984	Human mu-opioid re
8	69.4	97.7	2162	19	AAV61986	Human mu-opioid re
9	69.4	97.7	2162	19	AAV61987	Human mu-opioid re

10	69.4	97.7	2162	19	AAV61988	Human mu-opioid re
11	69.4	97.7	2162	19	AAV61989	Human mu-opioid re
12	69.4	97.7	2162	19	AAV61991	Human mu-opioid re
13	69.4	97.7	2162	19	AAV61992	Human mu-opioid re
14	69.4	97.7	2162	19	AAV61993	Human mu-opioid re
15	69.4	97.7	2162	19	AAV61994	Human mu-opioid re
16	69.4	97.7	2162	19	AAV61995	Human mu-opioid re
17	69.4	97.7	2162	21	AAZ88470	Human mu-opioid re
18	67.8	95.5	2162	19	AAV61990	Human mu-opioid re
19	56.6	79.7	1334	21	AAZ60738	cDNA encoding muri
20	56.6	79.7	1346	21	AAZ60737	cDNA encoding muri
21	56.6	79.7	1365	21	AAZ60736	cDNA encoding muri
22	56.6	79.7	1423	21	AAZ60726	cDNA encoding muri
23	56.6	79.7	1542	21	AAZ60729	cDNA encoding muri
24	56.6	79.7	1610	21	AAZ60741	cDNA encoding muri
25	56.6	79.7	1618	16	AA089222	Rat mu oploid rece
26	56.6	79.7	1618	16	AA089223	Transcription regu
27	56.6	79.7	1618	21	AA059499	cDNA encoding a mu
28	56.6	79.7	1729	21	AAZ60734	cDNA encoding muri
29	56.6	79.7	2045	21	AAZ60735	cDNA encoding muri
30	56.6	79.7	2135	22	AAZ60735	Nucleotide sequenc
31	56.6	79.7	2229	19	AAV49252	Mouse mu opiate re
32	53.4	75.2	1981	15	AA056705	Partial sequence o
33	53.4	75.2	1981	22	AA011041	Murine delta opioi
34	49.2	69.3	6494	24	ABL33393	Human immune syste
35	44.6	62.8	2070	15	AA079199	Rat mu-subtype opi
36	37.4	52.7	6494	24	ABL33392	Human immune syste
37	26.4	37.2	109519	22	AAZ08693	Micromonospora DNA
38	25.6	36.1	527	22	AAK93041	Human cDNA 3'-end
39	25.6	36.1	1178	21	AAK90469	Human uncoupling P
40	25.6	36.1	1856	22	AA160768	Human polynucleoti
41	25.6	36.1	1872	22	AAK94578	Human full-length
42	25.6	36.1	2003	22	AA158982	Human polynucleoti
43	25.6	36.1	2004	22	AA127736	Human transport pr
44	25.4	35.8	1634	22	AAK32771	Human secreted pro
45	25.4	35.8	2853	21	AAA28683	DNA encoding JEST,
46	25	35.2	16018	22	AAK35884	Human cardiovascular
47	24.8	34.9	402	22	AA189669	Human polynucleoti
48	24.8	34.9	2053	21	AAK77724	Human cancer assoc
49	24.8	34.9	2190	20	AAZ24407	Human bladder tumo
50	24.8	34.9	4351	21	AAZ48077	Human insulin like
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53	24.2	34.1	1878	22	AAK94404	Human full-length
54	24.2	34.1	1877	22	AAH17890	Human cDNA sequenc
55	24.2	34.1	2439	18	AAK84456	Nucleotide sequenc
56	24.2	34.1	4804	20	AAK86375	Chicken embryo let
57	24.2	34.1	4804	20	AAK26690	Complete genome se
58	24.2	34.1	44018	22	AAK82392	Avian adenovirus C
59	24	33.8	367	19	AAV26648	Human PS12 DNA fr
60	24	33.8	367	21	AAA64082	Partial sequence g
61	24	33.8	410	21	AAA49928	Human putative cal
62	24	33.8	1495	22	AAH99540	Human protein enco
63	24	33.8	1524	19	AAV61200	Full length cDNA s
64	24	33.8	1524	24	AA058585	Prostate tumour sp
65	24	33.8	1524	21	AA063348	Human immunogenic
66	24	33.8	1524	22	AAZ63555	Human prostate CDN
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71	24	33.8	1524	22	AAH02529	Prostate tumour an
72	24	33.8	1987	24	AAK94302	Human full-length
73	24	33.8	2180	21	AAA49921	Human calcium chan
74	24	33.8	2393	19	AAV26656	Human PS12 consen
75	24	33.8	2393	21	AAA64090	Consensus sequence
76	24	33.8	3387	22	AAH76384	Human TLCC polyep
77	24	33.8	3901	22	AAH76383	Human TLCC polyep
78	24	33.8	4061	21	AAA49923	Human calcium chan
79	24	33.8	5157	22	AAZ36240	Human musculoskele
80	23.8	33.5	303	22	AAH08699	M. carbonacea DNA
81	23.8	33.5	553	11	AAO03735	Myocardacterium tube
82	23.8	33.5	597	22	AAK25023	MPB-57 protein enc
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C 84	23.8	33.5	2181	20	AAK07446	Rhodothermus marin	C 157	22.8	32.1	885	22	AAK26439	Pseudomonas sp hea
C 85	23.8	33.5	2181	21	AAZ89961	Isozymylase nucleot	C 158	22.8	32.1	1281	13	AAO23296	HSV-1 (MGH-10) ICP
C 86	23.8	33.5	2376	20	AAK16153	Mouse Sox1 cDNA.	C 159	22.8	32.1	1303	13	AAO23297	HSV-1 (CWS-2) ICP3
C 87	23.8	33.5	2802	20	AAK52420	Human polynucleoti	C 160	22.8	32.1	1335	13	AAO23295	HSV-1 (F) ICP34.5
C 88	23.8	33.5	3024	23	ABLI17103	Drosophila melanog	C 161	22.8	32.1	2208	21	AAK21847	Human breast and o
C 89	23.8	33.5	5654	23	ABLI17102	Drosophila melanog	C 162	22.8	32.1	10820	22	ABAI16598	Human nervous syst
C 90	23.8	33.5	24533	22	AAK27689	DNA encoding novel	C 163	22.8	32.1	50341	19	AAK26574	DNA sequence of a
C 91	23.6	33.2	390	22	AAK64253	Novel human polynu	C 164	22.8	32.1	50341	21	AAK39519	L5 shuttle phasmid
C 92	23.6	33.2	415	21	AAK30086	Human colon cancer	C 165	22.8	32.1	52297	16	AAK51411	Mycobacteriophage
C 93	23.6	33.2	421	22	AAK34846	Human colon cancer	C 166	22.8	32.1	52298	14	AAK47357	L5 mycobacteriopho
C 94	23.6	33.2	488	22	AAK90057	Human polynucleoti	C 167	22.8	32.1	58857	21	AAK58471	Nucleotide sequenc
C 95	23.6	33.2	2156	18	AAK90384	Human MIP-1-alpha/	C 168	22.8	32.1	4403765	22	AAK199683	Mycobacterium tube
C 96	23.6	33.2	2156	21	AAK21258	Human low adenosin	C 169	22.8	32.1	4411529	22	AAK199682	Mycobacterium tube
C 97	23.6	33.2	2156	21	AAK21262	Human low adenosin	C 170	22.8	31.8	650	22	ABK08983	Human polynucleoti
C 98	23.6	33.2	2156	21	AAK35136	Human adenosine re	C 171	22.6	31.8	1388	22	AAK59039	Human IF-gamma rec
C 99	23.6	33.2	2156	21	AAK35140	Human adenosine re	C 172	22.6	31.8	1388	22	AAK59039	Human secreted pro
C 100	23.6	33.2	6606	21	AAK21265	Human low adenosin	C 173	22.6	31.8	1495	15	AAK62695	C-C chemokine rece
C 101	23.6	33.2	6606	21	AAK35143	Human adenosine re	C 174	22.6	31.8	1495	15	AAK21264	Human low adenosin
C 102	23.4	33.0	412	21	AAK82265	N. meningitidis pa	C 175	22.6	31.8	1495	21	AAK35142	Human adenosine re
C 103	23.4	33.0	412	22	AAK35513	Human musculoskele	C 176	22.6	31.8	1512	22	AAK61103	P. putida KT2440-a
C 104	23.4	33.0	1199	22	AAK45021	CDNA encoding nove	C 177	22.6	31.8	1560	11	AAK02862	Part of plasmid ps
C 105	23.4	33.0	1306	22	AAK93806	Human polynucleoti	C 178	22.6	31.8	1760	21	AAK44674	Zea mays DNA fragm
C 106	23.4	33.0	1933	22	ABLI19239	Human polynucleoti	C 179	22.6	31.8	1812	22	ABK08345	Human secreted pro
C 107	23.4	33.0	3539	23	ABLI04436	Drosophila melanog	C 180	22.6	31.8	1812	22	AAK99327	Human protein enco
C 108	23.4	33.0	3921	23	ABLI1097	Drosophila melanog	C 181	22.6	31.8	2253	22	AAK25974	Matze actin depoly
C 109	23.4	33.0	3933	23	ABLI19238	Drosophila melanog	C 182	22.6	31.8	2442	22	AAK55148	Pseudomonas aerugi
C 110	23.4	33.0	4883	22	AAK79410	Human polynucleoti	C 183	22.6	31.8	2556	22	AAK159455	Human polynucleoti
C 111	23.4	33.0	44453	20	AAK23519	Human immune/haema	C 184	22.6	31.8	3438	22	AAK161241	Human polynucleoti
C 112	23.2	32.7	141	19	AAK46281	Human kidney amino	C 185	22.6	31.8	4522	20	AAK35965	Human int-1 mammar
C 113	23.2	32.7	227	20	AAK40856	C. reinhardtii por	C 186	22.6	31.8	5656	22	AAK25976	Matze ADF promoter
C 114	23.2	32.7	963	23	AAK89281	Human secreted pro	C 187	22.6	31.8	6030	22	AAK25977	Matze ADF promoter
C 115	23.2	32.7	969	23	AAK54056	Human brain T calc	C 188	22.6	31.8	6030	22	AAK25977	S. erythraea Oleand
C 116	23.2	32.7	1608	23	AAK85253	Pseudomonas aerugi	C 189	22.6	31.8	6939	20	AAK25775	Matze ADF promoter
C 117	23.2	32.7	1698	23	AAK54133	DNA encoding novel	C 190	22.6	31.8	7728	24	ABK32077	Human immune syste
C 118	23.2	32.7	1838	20	AAK32119	Pseudomonas aerugi	C 191	22.6	31.8	11365	22	AAK73827	Human immune/haema
C 119	23.2	32.7	1838	21	AAK45282	Chlamydomonas rein	C 192	22.6	31.8	13842	21	AAK87297	S. venezuelae macr
C 120	23.2	32.7	1838	22	ABK0286	Chlamydomonas ppo	C 193	22.6	31.8	20046	22	AAK73826	Human immune/haema
C 121	23.2	32.7	3118	22	AAK02863	Human nervous syst	C 194	22.6	31.8	30001	18	AAK61016	Total DNA sequence
C 122	23.2	32.7	3118	22	AAK03980	Human reproductive	C 195	22.6	31.8	30001	19	AAK05110	S. aureofaciens DN
C 123	23.2	32.7	4820	22	ABLI19637	Drosophila melanog	C 196	22.6	31.8	36519	19	AAK22141	Chimpanzee adenovi
C 124	23.2	32.7	6072	22	AAK42088	Genomic sequence #	C 197	22.6	31.8	36778	21	AAK87318	S. venezuelae ptk
C 125	23.2	32.7	6072	22	AAK05835	Human reproductive	C 198	22.6	31.8	37948	21	AAK87318	S. venezuelae ptk
C 126	23.2	32.7	6816	24	AAK16826	Human T-type calci	C 199	22.6	31.8	38506	21	AAK75633	Nucleotide sequenc
C 127	23.2	32.7	6855	24	AAK16827	Human T-type calci	C 200	22.6	31.8	38506	21	AAK75633	Recombinant cosmid
C 128	23.2	32.7	6933	23	AAK57141	DNA encoding novel	C 201	22.6	31.8	42717	22	AAK90032	Nucleotide sequenc
C 129	23.2	32.4	502	19	AAK61336	Extended cDNA seq	C 202	22.6	31.8	50937	21	AAK09469	Streptococcus olea
C 130	23.2	32.4	502	19	AAK58665	Prostate tumour sp	C 203	22.6	31.5	420	23	AAK76265	DNA encoding novel
C 131	23.2	32.4	502	21	AAK06428	Human immunogenic	C 204	22.4	31.5	420	23	AAK76265	DNA encoding novel
C 132	23.2	32.4	502	21	AAK63656	Human prostate cdn	C 205	22.4	31.5	633	22	AAK12793	Human breast cance
C 133	23.2	32.4	502	22	AAK10187	Human prostate tum	C 206	22.4	31.5	657	22	AAK93997	Human foetal cDNA,
C 134	23.2	32.4	502	22	AAK93544	Human prostate-spe	C 207	22.4	31.5	683	22	AAK12164	Human breast cance
C 135	23.2	32.4	502	22	AAK84858	Human prostate-spe	C 208	22.4	31.5	760	22	AAK18680	Human polynucleoti
C 136	23.2	32.4	502	22	AAK02609	Prostate tumour an	C 209	22.4	31.5	1004	22	AAK168176	Human hexose kinas
C 137	23.2	32.4	537	20	AAK87253	EST clone BN342.	C 210	22.4	31.5	1182	21	AAK75608	CDNA encoding a ch
C 138	23.2	32.4	516	23	AAK59353	DNA encoding novel	C 211	22.4	31.5	1452	21	AAK91047	Rat methadone-spec
C 139	23.2	32.4	1052	22	AAK529788	Human cytoskeletal	C 212	22.4	31.5	1574	10	AAK90599	Human lipocortin-V
C 140	23.2	32.4	1310	21	AAK58119	Human PRO1555 nucl	C 213	22.4	31.5	1695	22	AAK41655	CDNA encoding nove
C 141	23.2	32.4	1310	21	AAK37120	Human PRO1555 (UNO	C 214	22.4	31.5	1695	22	AAK35045	CDNA encoding nove
C 142	23.2	32.4	1362	21	AAK5438	DNA encoding prote	C 215	22.4	31.5	1705	22	AAK45082	CDNA encoding nove
C 143	23.2	32.4	1362	21	AAK69101	Human secreted pro	C 216	22.4	31.5	1735	22	AAK45270	CDNA encoding nove
C 144	23.2	32.4	1375	17	AAK90405	Actinomadura sp. D	C 217	22.4	31.5	2953	22	AAK68359	Human immune/haema
C 145	23.2	32.4	1375	18	AAK64930	Actinomadura flexu	C 218	22.4	31.5	2953	22	AAK68360	Human immune/haema
C 146	23.2	32.4	2001	22	AAK60958	P. putida KT2440-a	C 219	22.4	31.5	4226	21	AAK93780	Chicken-pox virus
C 147	23.2	32.4	2100	22	AAK98725	Human late stage c	C 220	22.4	31.5	4603	22	AAK78076	Human immune/haema
C 148	23.2	32.4	3460	23	AAK89518	DNA encoding novel	C 221	22.4	31.5	5103	22	AAK61193	Human polynucleoti
C 149	23.2	32.4	6649	22	AAK199418	Human excretory re	C 222	22.4	31.5	13744	22	AAK68361	Human immune/haema
C 150	23.2	32.4	6649	22	AAK163768	Human kidney relat	C 223	22.4	31.5	13744	22	AAK82406	Human immune/haema
C 151	23.2	32.4	12019	20	AAK18867	Alcaligenes sp. po	C 224	22.4	31.5	14049	22	ABK15812	Human nervous syst
C 152	23.2	32.4	349980	22	AAK64966	C glutamicum codin	C 225	22.4	31.5	42519	22	AAK81318	Human immune/haema
C 153	23.2	32.4	349980	22	AAK68525	C glutamicum codin	C 226	22.4	31.5	125157	22	AAK74202	Nucleotide sequenc
C 154	22.8	32.1	549	21	AAK66009	E. coli proliferat	C 227	22.2	31.3	338	22	AAK74202	Nucleotide sequenc
C 155	22.8	32.1	549	23	AAK52738	E. coli DNA for ce	C 228	22.2	31.3	338	22	AAK83230	Human polynucleoti

C 229	22.2	31.3	471	22	AAK63647	Human immune/haema	302	22	31.0	124884	22	AAH74201	Nucleotide sequenc
C 230	22.2	31.3	485	22	ABA42253	Human breast cell	C 303	22	31.0	124884	22	AAH74201	Nucleotide sequenc
C 231	22.2	31.3	485	22	ABA52678	Human foetal liver	C 304	22	31.0	349980	22	AAH68533	CDNA encoding novel
C 232	22.2	31.3	485	22	ABA22466	Probe #932 for gen	C 305	21.8	30.7	339	23	AAH59763	CDNA encoding novel
C 233	22.2	31.3	485	22	AAK00936	Human brain expres	C 306	21.8	30.7	361	21	AAH69767	Human ovarian carc
C 234	22.2	31.3	485	22	AAK26390	Human bone marrow	C 307	21.8	30.7	361	21	AAH69913	Human ovarian carc
C 235	22.2	31.3	485	22	AAI11022	Probe #955 for gen	C 308	21.8	30.7	361	21	AAH69914	Human ovarian carc
C 236	22.2	31.3	485	22	AAI32284	Probe #970 used to	C 309	21.8	30.7	380	22	ABA45273	Human breast cell
C 237	22.2	31.3	485	22	AAI00942	Probe #933 used to	C 310	21.8	30.7	380	22	ABA25445	Human breast cell
C 238	22.2	31.3	673	21	AAK97708	Brldge-1 related p	C 311	21.8	30.7	380	22	AAK03983	Human brain expres
C 239	22.2	31.3	682	21	AAK37215	Arabidopsis thalia	C 312	21.8	30.7	468	22	AAK25187	Human brain expres
C 240	22.2	31.3	706	20	AAH215277	Human gene express	C 313	21.8	30.7	468	22	AAH25236	Human ovarian tumo
C 242	22.2	31.3	1215	23	AAH52057	Mycobacterium tube	C 314	21.8	30.7	581	22	AAH83834	Human ovarian tumo
C 243	22.2	31.3	1323	23	AAH85260	DNA encoding novel	C 315	21.8	30.7	643	20	AAH69543	Human ovarian tumo
C 244	22.2	31.3	1343	22	ABA16862	Human nervous syst	C 316	21.8	30.7	647	20	AAH91458	P. neopollyactyla
C 245	22.2	31.3	1343	22	ABA19755	Human nervous syst	C 317	21.8	30.7	647	20	AAH91459	T. gondii immune
C 246	22.2	31.3	1761	21	AAH58473	Nucleotide sequenc	C 318	21.8	30.7	647	22	AAH42782	T. gondii ntG647 T
C 247	22.2	31.3	2068	22	ABA20372	Human nervous syst	C 319	21.8	30.7	647	22	AAH42782	Reverse complement
C 248	22.2	31.3	2139	23	AAH54180	Pseudomonas aerugi	C 320	21.8	30.7	860	22	AAH08247	Human cDNA clone (
C 249	22.2	31.3	2547	22	AAH93794	Human cDNA encodin	C 321	21.8	30.7	997	22	AAH94498	Human full-length
C 250	22.2	31.3	2834	8	AAH70307	Sequence of human	C 322	21.8	30.7	1008	22	AAH51988	Mycobacterium tube
C 251	22.2	31.3	2834	10	AAH90394	Genomic DNA of hum	C 323	21.8	30.7	1024	20	AAH33971	Human TIE ligand N
C 252	22.2	31.3	2834	16	AAQ92785	MIS human gene in	C 324	21.8	30.7	1024	21	AAH60538	Human TIE ligand N
C 253	22.2	31.3	3331	21	AAH75918	Human ORFX ORF1473	C 325	21.8	30.7	1024	22	AAH21401	Human cDNA sequenc
C 254	22.2	31.3	3405	23	AAH76983	DNA encoding novel	C 326	21.8	30.7	1024	22	AAH90565	Human cDNA sequenc
C 255	22.2	31.3	3426	20	AAH23819	Human SRBP-2 CDNA	C 327	21.8	30.7	1024	22	AAH97392	Human PDI19 CDNA.
C 256	22.2	31.3	3500	21	AAH74935	Human ORFX ORF490	C 328	21.8	30.7	1029	21	AAH64288	Human angiogenesis
C 257	22.2	31.3	3803	22	AAH60788	Human polynucleoti	C 329	21.8	30.7	1209	20	AAH74286	Human membrane-ass
C 258	22.2	31.3	3804	22	AAH59002	Human polynucleoti	C 330	21.8	30.7	1211	19	AAH34569	R. eutropha Mgt OR
C 259	22.2	31.3	5197	16	AAQ79038	Human SRBP-2 codi	C 331	21.8	30.7	1211	20	AAH211303	M. vaccae antigen
C 260	22.2	31.3	5962	23	AAH54522	Pseudophila melanog	C 332	21.8	30.7	1357	20	AAH70486	Chimeric PCB decomp
C 261	22.2	31.3	7347	23	AAH54136	Drosophila melanog	C 333	21.8	30.7	1471	20	AAH36137	DNA encoding human
C 262	22.2	31.3	12328	22	ABA20373	Human nervous syst	C 334	21.8	30.7	1508	22	AAH31010	Human diagnostic a
C 263	22.2	31.3	23823	22	AAK79160	Human immune/haema	C 335	21.8	30.7	1513	21	AAH59566	Human secreted pro
C 264	22.2	31.3	23825	22	AAK79161	Human immune/haema	C 336	21.8	30.7	1898	20	AAH40075	Colon cancer assoc
C 265	22.2	31.3	35048	23	ABL06102	Drosophila melanog	C 337	21.8	30.7	1898	23	AAH66871	DNA encoding novel
C 266	22.2	31.3	4411529	22	AAH96862	Mycobacterium tube	C 338	21.8	30.7	2129	22	ABA88920	Escherichia coli p
C 267	22.2	31.0	653	21	AAH06588	Human immunogenic	C 339	21.8	30.7	2191	21	AAH88502	Human protein kina
C 268	22.2	31.0	653	22	AAH63797	Human prostate CDN	C 340	21.8	30.7	2524	21	AAH82863	Human polynucleoti
C 269	22.2	31.0	653	22	AAH93704	Human prostate-spe	C 341	21.8	30.7	2531	22	AAH51879	Human polynucleoti
C 270	22.2	31.0	653	22	AAH85018	Human prostate-spe	C 342	21.8	30.7	2625	22	AAH26354	P. putida oxygenas
C 271	22.2	31.0	713	21	AAH02769	Prostate tumour an	C 343	21.8	30.7	2801	22	AAH26992	CDNA encoding nove
C 272	22.2	31.0	713	21	AAH08097	Hepatitis type C v	C 344	21.8	30.7	3397	22	AAH60273	Human polynucleoti
C 273	22.2	31.0	734	22	AAH07713	Human cDNA clone (C 345	21.8	30.7	3510	23	AAH66874	DNA encoding novel
C 274	22.2	31.0	792	12	AAH48413	Arabidopsis thalia	C 346	21.8	30.7	3557	22	ABA83109	HOSR-1 ovarian tum
C 275	22.2	31.0	836	12	AAO12218	SMUC-41 intestinal	C 347	21.8	30.7	3557	22	AAH18638	Human cDNA sequenc
C 276	22.2	31.0	1104	23	ABL26081	Drosophila melanog	C 348	21.8	30.7	3557	22	AAH18638	Human matrix-type
C 277	22.2	31.0	1134	22	AAH68035	C glutaminc codin	C 349	21.8	30.7	3695	20	AAH59403	CDNA encoding chic
C 278	22.2	31.0	1641	23	AAH73131	DNA encoding novel	C 350	21.8	30.7	3991	24	AAH16274	DNA encoding novel
C 279	22.2	31.0	1754	22	AAH14926	Human cDNA sequenc	C 351	21.8	30.7	4142	19	AAH62750	Human secreted pro
C 280	22.2	31.0	2307	22	AAH59307	Human polynucleoti	C 352	21.8	30.7	4326	23	AAH69668	DNA encoding novel
C 281	22.2	31.0	2888	22	ABL16825	Drosophila melanog	C 353	21.8	30.7	5751	22	AAH51986	Human polynucleoti
C 282	22.2	31.0	2898	22	AAH50867	Human cancer agent	C 354	21.8	30.7	7535	22	AAH18487	Human polynucleoti
C 283	22.2	31.0	2898	22	AAH50868	Human cancer agent	C 355	21.8	30.7	7620	22	ABA07349	Human pancreatic c
C 284	22.2	31.0	3170	23	ABL26080	Drosophila melanog	C 356	21.8	30.7	7620	22	AAH32776	Human genomic DNA
C 285	22.2	31.0	3294	22	AAH57441	Human intestine ce	C 357	21.8	30.7	9549	22	AAH53175	Human purified sec
C 286	22.2	31.0	4011	15	AAO70362	Varicella zoster v	C 358	21.8	30.7	15355	22	AAH57405	Human skeletal mus
C 287	22.2	31.0	4011	15	AAO66981	DNA encoding vZY I	C 359	21.8	30.7	15359	22	ABA80724	Human tyandoline re
C 288	22.2	31.0	6114	20	AAH83490	Human T-type volta	C 360	21.8	30.7	15359	22	ABA80724	DNA encoding novel
C 289	22.2	31.0	6132	20	AAH83489	Human T-type volta	C 361	21.8	30.7	15359	22	ABA80724	Ryanodine receptor
C 290	22.2	31.0	6690	23	AAH16769	Drosophila melanog	C 362	21.8	30.7	16026	12	AAH11415	Human nervous syst
C 291	22.2	31.0	7549	22	AAH32737	Human nervous syst	C 363	21.8	30.7	17514	22	AAH16260	Human nervous syst
C 292	22.2	31.0	7549	22	AAH32738	Human genomic DNA	C 364	21.8	30.7	18522	23	AAH59560	Human immune/haema
C 293	22.2	31.0	9839	22	AAH90502	Human genomic DNA	C 365	21.8	30.7	19115	22	ABA16261	Propionibacterium
C 294	22.2	31.0	9839	22	AAH90502	Human excretory re	C 366	21.8	30.7	19115	22	ABA16261	Human nervous syst
C 295	22.2	31.0	9968	22	AAH16353	Human kidney relat	C 367	21.8	30.7	30690	21	AAH92301	S. avermilitis ave
C 296	22.2	31.0	15720	22	AAH129504	Human musculoskele	C 368	21.8	30.7	30690	22	AAH92301	Streptomyces averm
C 297	22.2	31.0	19861	22	AAH71206	C899P determined c	C 369	21.8	30.4	37716	23	AAH90553	Propionibacterium
C 298	22.2	31.0	29139	23	AAH59569	Human immune/haema	C 370	21.6	30.4	504	22	AAH90700	Human MANGO 349 CD
C 299	22.2	31.0	47670	23	AAH59569	Propionibacterium	C 371	21.6	30.4	504	22	AAH90701	Human MANGO 349 T2
C 300	22.2	31.0	50368	23	ABL16788	Drosophila melanog	C 372	21.6	30.4	504	22	AAH90702	Human MANGO 349 R2
C 301	22.2	31.0	50937	21	AAH09469	Streptococcus olea	C 373	21.6	30.4	504	22	AAH90703	Human MANGO 349 E4
C 302	22.2	31.0	109519	22	AAH08693	Micromonospora DNA	C 374	21.6	30.4	565	21	AAH08704	Fusarium venenatum

c 375	21.6	30.4	566	22	AAH10007	Human cDNA clone (c 448	21.4	30.1	566	22	ABA31339	Probe #9805 for ge
376	21.6	30.4	630	23	ABLO6637	Drosophila melanog	c 449	21.4	30.1	566	22	AAK12668	Human brain expres
377	21.6	30.4	679	23	AAH16843	Human cDNA clone (c 450	21.4	30.1	566	22	AAK38385	Human bone marrow
378	21.6	30.4	801	22	AAI97433	Human neuroblastom	c 451	21.4	30.1	566	22	AAI19182	Probe #9115 for ge
c 379	21.6	30.4	880	21	AAA26718	Candida albicans p	c 452	21.4	30.1	566	22	AAI44340	Probe #13026 used
380	21.6	30.4	903	23	AAAS83666	DNA encoding novel	c 453	21.4	30.1	573	18	AAV06338	Recombinant protei
381	21.6	30.4	903	23	AAAS92437	DNA encoding novel	c 454	21.4	30.1	766	21	AAE12111	Aspergillus oryzae
382	21.6	30.4	1027	14	AAQ43452	Sequence of endoce	c 455	21.4	30.1	950	23	AAAS80936	DNA encoding novel
383	21.6	30.4	1032	21	AAA12986	DNA encoding strep	c 456	21.4	30.1	888	22	AAK86183	Human immune/haema
384	21.6	30.4	1212	22	AAAS23237	DNA encoding novel	c 457	21.4	30.1	1016	17	AAAT29401	Lipase coding sequ
385	21.6	30.4	1422	22	AAAS23150	DNA encoding novel	c 458	21.4	30.1	1027	23	AAAS68733	DNA encoding novel
386	21.6	30.4	1548	20	AAAX20523	Polyomavirus seq	c 459	21.4	30.1	1037	23	AAAC58901	Human tumor suppr
c 387	21.6	30.4	1549	16	AAQ88151	Xanthomonas L-glut	c 460	21.4	30.1	1176	21	AACT78151	Human cancer assoc
388	21.6	30.4	1791	24	AAAS62454	CDNA sequence #241	c 461	21.4	30.1	1368	23	ABLO29339	Drosophila melanog
c 389	21.6	30.4	1831	21	AAAZ7487	5' HB5 endogenous r	c 462	21.4	30.1	1366	23	AAAS59774	Propionibacterium
390	21.6	30.4	1958	22	AAH18689	Human cDNA sequenc	c 463	21.4	30.1	1541	22	AAAF82082	Human aldehyde deh
c 391	21.6	30.4	2006	15	AAO50147	Phospholipase D-p	c 464	21.4	30.1	1628	22	AAH14704	Human cDNA sequenc
392	21.6	30.4	2110	20	AAV84610	Human secreted pro	c 465	21.4	30.1	1651	24	ABJ34326	Human immune syste
c 393	21.6	30.4	2110	22	ABAB8393	Human secreted pro	c 466	21.4	30.1	1709	22	AAK51755	DNA encoding novel
c 394	21.6	30.4	2255	21	AAAT72387	Human nucleic acid	c 467	21.4	30.1	1851	23	AAAS82716	DNA encoding novel
c 395	21.6	30.4	2281	22	AAAF98709	Human late stage o	c 468	21.4	30.1	1873	22	AAK94604	Human full-length
c 396	21.6	30.4	2286	20	AAAX01152	M. tuberculosis an	c 469	21.4	30.1	1945	22	AAK52739	Human polynucleoti
c 397	21.6	30.4	2286	20	AAAX01186	M. tuberculosis an	c 470	21.4	30.1	2036	20	AAZ33590	Human breast tumor
c 398	21.6	30.4	2286	20	AAAS12464	Mycobacterium tube	c 471	21.4	30.1	2036	20	AAZ33590	Human breast tumor
c 399	21.6	30.4	2533	23	AAAS85490	DNA encoding novel	c 472	21.4	30.1	2071	21	AAAF18274	Lung cancer associ
c 400	21.6	30.4	2533	19	AAV46297	C. reinhardtii pro	c 473	21.4	30.1	2167	21	AAZ38338	Human keratin KRT
c 401	21.6	30.4	2674	23	ABL22498	Drosophila melanog	c 474	21.4	30.1	2172	22	AAH02956	Human shear stress
c 402	21.6	30.4	2742	19	AAV49291	Aujesky's disease	c 475	21.4	30.1	2240	21	AAA26419	Human secreted pro
c 403	21.6	30.4	2771	22	AAH17350	Human cDNA sequenc	c 476	21.4	30.1	2286	20	AAAX01152	M. tuberculosis an
c 404	21.6	30.4	2796	6	AAAS0036	Partial sequence o	c 477	21.4	30.1	2286	20	AAAX01186	Mycobacterium tube
c 405	21.6	30.4	2878	23	ABLO6636	Drosophila melanog	c 478	21.4	30.1	2286	22	AAAS12464	Mycobacterium tube
c 406	21.6	30.4	3061	23	ABLI18181	Drosophila melanog	c 479	21.4	30.1	2389	22	ABA08617	Human secreted pro
c 407	21.6	30.4	3107	20	AAV68092	CDNA encoding the	c 480	21.4	30.1	2586	22	AAH65421	C glutamic codin
c 408	21.6	30.4	3126	23	ABLO5238	Drosophila melanog	c 481	21.4	30.1	2703	22	AAK71587	Human immune/haema
c 409	21.6	30.4	3381	19	AAV46298	C. reinhardtii pro	c 482	21.4	30.1	2802	23	AAAS54083	Pseudomonas aerugi
c 410	21.6	30.4	3649	22	AAV90654	Human MANGO 349 cd	c 483	21.4	30.1	2817	19	AAV01590	Rat glycine transp
c 411	21.6	30.4	4115	21	AAAG97430	Gluconobacter oxyd	c 484	21.4	30.1	2925	22	AAH16388	Human cDNA sequenc
c 412	21.6	30.4	4136	23	AAAS91287	DNA encoding novel	c 485	21.4	30.1	3120	22	AAAC85694	Nucleotide sequenc
c 413	21.6	30.4	4321	23	ABLI14517	Drosophila melanog	c 486	21.4	30.1	3349	22	AAAS03079	Human diagnostic a
c 414	21.6	30.4	4480	18	AAAT71260	Rat sarcoma virus	c 487	21.4	30.1	3562	22	ABAI17959	Human nervous syst
c 415	21.6	30.4	4480	21	AAAG60823	Nucleotide sequenc	c 488	21.4	30.1	3754	20	AAAS59767	SEQ ID 6 of W09919
c 416	21.6	30.4	4647	23	ABLO7574	Drosophila melanog	c 489	21.4	30.1	4056	23	AAAS85408	DNA encoding novel
c 417	21.6	30.4	4897	11	AAO03259	Drosophila melanog	c 490	21.4	30.1	4114	23	ABLO2938	Drosophila melanog
c 418	21.6	30.4	5918	22	AAAS32541	Pseudotubercles virus	c 491	21.4	30.1	4856	23	ABLO2938	Drosophila melanog
c 419	21.6	30.4	6204	23	ABLI18180	Human genomic DNA	c 492	21.4	30.1	5545	23	ABLO2944	Drosophila melanog
c 420	21.6	30.4	7405	22	AAK83850	Drosophila melanog	c 493	21.4	30.1	5874	22	AAAS59765	CDNA encoding huma
c 421	21.6	30.4	7421	23	AAK89313	Human immune/haema	c 494	21.4	30.1	6058	22	AALO2805	Human reproductive
c 422	21.6	30.4	7632	22	AAAS85482	Human digestive sy	c 495	21.4	30.1	6941	20	AAAS9082	Human activated ca
c 423	21.6	30.4	8895	22	AAAS32714	Human genomic DNA	c 496	21.4	30.1	7898	20	AAAS9080	Human activated ca
c 424	21.6	30.4	8895	22	AAK91538	Human digestive sy	c 497	21.4	30.1	7898	20	AAAS9081	Human activated ca
c 425	21.6	30.4	8895	22	AAI57795	Human colorectal c	c 498	21.4	30.1	8232	22	AAK71585	Human immune/haema
c 426	21.6	30.4	8896	22	AAAS32712	Human genomic DNA	c 499	21.4	30.1	8350	22	AAAS41703	Genomic sequence #
c 427	21.6	30.4	8896	22	AAK91537	Human digestive sy	c 500	21.4	30.1	8615	22	ABAI14693	Human nervous syst
c 428	21.6	30.4	8896	22	AAI57794	Human colorectal c	c 501	21.4	30.1	8615	22	ABAI14694	Human nervous syst
c 429	21.6	30.4	9101	23	ABLI14516	Human colorectal c	c 502	21.4	30.1	9359	22	AAK73225	Human immune/haema
c 430	21.6	30.4	11372	22	AAK70526	Drosophila melanog	c 503	21.4	30.1	12221	22	AAK71585	Human immune/haema
c 431	21.6	30.4	12113	24	AAAS17492	Human immune/haema	c 504	21.4	30.1	12221	22	AAK71585	Human immune/haema
c 432	21.6	30.4	13380	24	AAAS19637	Human acetylcholin	c 505	21.4	30.1	19088	24	ABA94451	Human corticostero
c 433	21.6	30.4	14209	22	AAK89137	Propionibacterium	c 506	21.4	30.1	21596	22	AAK71582	Human immune/haema
c 434	21.6	30.4	14209	22	AAK89137	Human digestive sy	c 507	21.4	30.1	53789	19	AAV21187	Human immune/haema
c 435	21.6	30.4	32177	22	ABAI18493	Human digestive sy	c 508	21.4	30.1	77536	21	AAAI14651	Nucleotide sequenc
c 436	21.6	30.4	32177	22	AAAS29628	Human nervous syst	c 509	21.4	30.1	114855	20	AAK53491	Human adenosine Ai
c 437	21.6	30.4	32177	22	AAAS29628	Human cytoskeletal	c 510	21.4	30.1	349980	22	AAH68525	C glutamicum codin
c 438	21.6	30.4	32177	22	AAI05374	Human reproductive	c 511	21.2	29.9	50	22	AAI77649	Human silent SNP c
c 439	21.6	30.4	4403765	22	AAI90201	Human yes1 gene.	c 512	21.2	29.9	179	14	AAH27136	Exon/intron repair co
c 440	21.4	30.1	450	18	AAV06336	Mycobacterium tube	c 513	21.2	29.9	290	14	AAO63365	Human brain expres
c 441	21.4	30.1	455	18	AAV06336	Hepatitis C virus	c 514	21.2	29.9	342	20	AAK51945	Human secreted pro
c 442	21.4	30.1	478	16	AAI19890	CDNA encoding nove	c 515	21.2	29.9	404	23	AAAS79528	DNA encoding novel
c 443	21.4	30.1	528	18	AAV06343	Human gene signatu	c 516	21.2	29.9	422	23	AAAS79529	DNA encoding novel
c 444	21.4	30.1	533	18	AAV06343	Mouse prolactin 1	c 517	21.2	29.9	543	22	AAH97799	Murine 7-transmemb
c 445	21.4	30.1	551	22	AAK93074	Target nucleci aci	c 518	21.2	29.9	543	22	AAH97799	Murine 7-transmemb
c 446	21.4	30.1	565	22	AAK93074	Human cDNA 3'-end	c 519	21.2	29.9	600	22	AAH06070	Human cDNA clone (
c 447	21.4	30.1	566	22	ABA64189	Human breast cancer	c 520	21.2	29.9	627	22	AAK79531	DNA encoding novel
						Human foetal liver				634	23	AAK57480	Human immune/haema

521	21.2	29.9	639	23	AA575935	DNA encoding novel	594	21.2	29.9	37736	22	AAK86139	Human immune/haema
522	21.2	29.9	660	20	AA586008	DNA encoding a gyr	595	21.2	29.9	65140	22	AAD17184	Streptomyces nous
523	21.2	29.9	677	21	AA613916	Aspergillus oryzae	596	21.2	29.9	125401	22	AAD17186	Streptomyces nous
524	21.2	29.9	701	16	AA076209	HSV L/ST ORF1. He	597	21.2	28.9	534720	19	AAV30458	Rhizobium species
525	21.2	29.9	712	22	AA531514	Human DNA for a no	598	21.2	29.9	536165	19	AAV30459	Rhizobium species
526	21.2	29.9	747	22	AA508464	Fusarium venenatum	599	21.2	29.9	1830121	17	AA142063	Haemophilus Influe
527	21.2	29.9	792	22	AA196336	Human neuroblastom	600	21	29.6	158	22	ABA75016	Human brain expres
528	21.2	29.9	801	22	AA197509	Human neuroblastom	601	21	29.6	158	22	ABA75016	Human brain expres
529	21.2	29.9	847	22	AA160675	Human polynucleoti	602	21	29.6	158	22	ABA33703	Probe #18169 for g
530	21.2	29.9	857	22	AA120041	Human breast cance	603	21	29.6	158	22	AAK23526	Human brain expres
531	21.2	29.9	906	21	AAA26407	Human secreted pro	604	21	29.6	158	22	AAK49658	Human bone marrow
532	21.2	29.9	910	22	AA158889	Human polynucleoti	605	21	29.6	158	22	AAI26766	Probe #16699 for g
533	21.2	29.9	953	22	AA510662	Rat GFRA1pha-4 spl	606	21	29.6	158	22	AA155543	Probe #24229 used
534	21.2	29.9	1008	22	AA513063	Rat GFRA1pha-4 spl	607	21	29.6	279	20	AAV89544	EST clone CR1135.
535	21.2	29.9	1023	23	AA554245	Pseudomonas aerugi	608	21	29.6	297	20	AAV89544	Genetic suppressor
536	21.2	29.9	1074	23	AA571558	DNA encoding novel	609	21	29.6	351	21	AA258778	Human huntingtin-1
537	21.2	29.9	1248	22	AA590937	Human I-beta-1,3-N	610	21	29.6	373	21	AAAC61555	Genetic suppressor
538	21.2	29.9	1256	23	AA580551	Drosophila melanog	611	21	29.6	386	22	AA565986	Novel human polynu
539	21.2	29.9	1281	21	AAA64852	Bordetella pertuss	612	21	29.6	492	22	AA565738	Novel human polynu
540	21.2	29.9	1446	23	AB113517	Drosophila melanog	613	21	29.6	400	21	AAAC61562	Genetic suppressor
541	21.2	29.9	1461	22	AA594439	Human hydrophobic	614	21	29.6	423	21	AAA31674	Plant microsatelli
542	21.2	29.9	1593	22	AA591989	Murine T-bet codin	615	21	29.6	432	22	AAH34220	Human colon cancer
543	21.2	29.9	1608	22	AA591988	Human T-bet codin	616	21	29.6	442	22	ABAI2073	Human nervous syst
544	21.2	29.9	1722	23	AA580551	DNA encoding novel	617	21	29.6	492	22	AA575840	Human OREF ORF1395
545	21.2	29.9	1728	23	AA552506	E. coli DNA for ce	618	21	29.6	502	22	ABA82610	Human Zmax 1 PCR p
546	21.2	29.9	1735	22	AA104953	Human reproductive	619	21	29.6	524	21	AAAC61554	Genetic suppressor
547	21.2	29.9	1758	22	AA594449	Human hydrophobic	620	21	29.6	531	22	ABA62493	Human foetal liver
548	21.2	29.9	1923	22	AA559861	Human novel cytol	621	21	29.6	531	22	ABA29824	Probe #4290 for ge
549	21.2	29.9	1940	22	AA594497	Human novel cytol	622	21	29.6	531	22	AAK10844	Human brain expres
550	21.2	29.9	1968	21	AA556211	Human cDNA, SEQ ID	623	21	29.6	531	22	AAK36706	Human bone marrow
551	21.2	29.9	2011	20	AA599465	Salmonella typhi D	624	21	29.6	531	22	AA117559	Probe #1792 for ge
552	21.2	29.9	2019	21	AA591188	Beta 1,3-N-acetyl	625	21	29.6	531	22	AA142472	Probe #1158 used
553	21.2	29.9	2175	22	AA555849	DNA encoding novel	626	21	29.6	535	22	AAK11847	Human brain expres
554	21.2	29.9	2175	22	AA555849	Mitomycin biosynth	627	21	29.6	535	22	AAK11847	Human brain expres
555	21.2	29.9	2214	17	AA528807	Amtidase family pro	628	21	29.6	535	22	AAK11847	Human breast cance
556	21.2	29.9	2385	21	AAA33981	Human G-protein co	629	21	29.6	630	21	AAAC50089	Human brain expres
557	21.2	29.9	2413	22	AAH15635	Human cDNA sequenc	630	21	29.6	635	21	AA577094	DNA encoding novel
558	21.2	29.9	2418	21	AAH33979	Human TANGO 187-2	631	21	29.6	641	8	AA577094	Interferon-induced
559	21.2	29.9	2464	22	AAH17900	Human cDNA sequenc	632	21	29.6	687	23	AA583337	DNA encoding novel
560	21.2	29.9	2490	21	AAA33975	Human TANGO 187-1	633	21	29.6	736	21	AAA46615	Human nervous syst
561	21.2	29.9	2523	21	AAA33978	Human TANGO 187-1	634	21	29.6	783	17	AAK03651	31-O-desmethyl-FK5
562	21.2	29.9	2524	24	AA599908	Polynucleotide enc	635	21	29.6	823	21	AA571279	Aspergillus oryzae
563	21.2	29.9	2552	21	AAA33980	Human TANGO 187-3	636	21	29.6	940	22	AA109960	Human breast cance
564	21.2	29.9	2595	21	AAA33976	Human TANGO 187-2	637	21	29.6	1001	21	AAH51516	Human UGT2B10 rela
565	21.2	29.9	2639	14	AAO41259	Human TANGO 187-2	638	21	29.6	1066	22	AA190707	Human polynucleoti
566	21.2	29.9	2639	15	AAO72718	2,2-dialkylglycine	639	21	29.6	1082	23	AA565697	DNA encoding novel
567	21.2	29.9	2700	21	AAA33977	Dialkylglycine dec	640	21	29.6	1150	17	AA503650	31-O-desmethyl-FK5
568	21.2	29.9	3219	23	AA574721	Human TANGO 187-1	641	21	29.6	1242	23	AA572110	Drosophila melanog
569	21.2	29.9	3267	23	AB117571	DNA encoding novel	642	21	29.6	1425	21	AAZ51983	Mouse Plox2b nucle
570	21.2	29.9	3567	23	AB113516	Drosophila melanog	643	21	29.6	1604	21	AAZ51983	Human nervous syst
571	21.2	29.9	4157	23	AB106835	Drosophila melanog	644	21	29.6	1806	22	ABAI5642	Human nervous syst
572	21.2	29.9	4424	22	AAK51737	Human polynucleoti	645	21	29.6	1854	20	AAK33296	M. grisea PTH11 ge
573	21.2	29.9	4504	22	AAK52721	Human polynucleoti	646	21	29.6	1960	20	AAZ20931	Human MUC18 cDNA s
574	21.2	29.9	4504	22	AAK52721	Haemophilus influe	647	21	29.6	1962	20	AAZ20932	Human MUC18 cDNA s
575	21.2	29.9	5519	20	AAK24981	Haemophilus influe	648	21	29.6	1971	22	AAZ68135	C glutaminc codin
576	21.2	29.9	5561	23	AB117570	Drosophila melanog	649	21	29.6	2086	22	AA527113	CDNA encoding nove
577	21.2	29.9	6943	22	AA542087	Genomic sequence #	650	21	29.6	2265	21	AA545625	Arabidopsis thalia
578	21.2	29.9	7029	24	AA517119	Ketoglucuronidase	651	21	29.6	2271	23	AA586441	DNA encoding novel
579	21.2	29.9	7312	23	AB105852	Drosophila melanog	652	21	29.6	2361	22	AA527490	DNA encoding nove
580	21.2	29.9	8011	23	AB106834	Drosophila melanog	653	21	29.6	2364	18	AAI36359	Asb2ya gossypii is
581	21.2	29.9	9045	22	AA506332	DNA encoding seven	654	21	29.6	2397	21	AAZ46408	Aspergillus oryzae
582	21.2	29.9	9087	22	AAAD14986	Human NOV7 DNA. H	655	21	29.6	2475	22	AAH84578	E. coli growth and
583	21.2	29.9	11389	22	AA559825	Human novel cytol	656	21	29.6	2547	14	AAO372238	C. melassecola ATCC
584	21.2	29.9	11604	22	AAAD14501	Streptomyces clav	657	21	29.6	2651	20	AAK33952	Human HCMV Inducib
585	21.2	29.9	11839	23	AB114261	Drosophila melanog	658	21	29.6	2686	22	AA513465	DNA encoding human
586	21.2	29.9	12001	16	AAO76213	HSV L/ST region.	659	21	29.6	2720	19	AA510464	S. capsulata proly
587	21.2	29.9	15044	22	AA536290	Human cardiovascular	660	21	29.6	2835	22	AAK86547	Human immune/haema
588	21.2	29.9	15046	22	AA536291	Human cardiovascular	661	21	29.6	2887	21	AA539014	Human pancreatic c
589	21.2	29.9	15079	16	AAO91580	S. clavuligerus cl	662	21	29.6	2949	23	AA567904	DNA encoding novel
590	21.2	29.9	15079	16	AAO91580	Streptomyces clavu	663	21	29.6	2949	23	AA567904	Human GTP-binding
591	21.2	29.9	18034	21	AA55841	Complete Mitomycin	664	21	29.6	3215	22	AAO13643	Human protein phos
592	21.2	29.9	23333	23	AB114260	Drosophila melanog	665	21	29.6	3247	22	AAD11946	Human protein phos
593	21.2	29.9	35026	21	AAA64890	Bordetella pertuss	666	21	29.6	3293	22	AAH02921	Human shear stress

c 667	21	29.6	3437	22	AAK52235	Human polynucleoti
c 668	21	29.6	3787	23	AA584930	DNA encoding novel
c 669	21	29.6	3835	20	AA32295	M. grisea PTH1 ge
c 670	21	29.6	4287	24	AA597177	Human metallopept
c 671	21	29.6	4351	19	AAV70397	LRP5 isoform 2 lon
c 672	21	29.6	4509	20	AA330081	Human ATP-binding
c 673	21	29.6	4511	22	AAAD16259	Human ATP-binding
c 674	21	29.6	4512	22	AAAD16231	Human ATP-binding
c 675	21	29.6	4512	22	AAAD16256	Human ATP-binding
c 676	21	29.6	4512	22	AAAD16257	Human ATP-binding
c 677	21	29.6	4512	22	AAAD16258	Human ATP-binding
c 678	21	29.6	4512	22	AAAD16260	Human ATP-binding
c 679	21	29.6	4512	22	AAAD16261	Human ATP-binding
c 680	21	29.6	4512	22	AAAD16262	Human ATP-binding
c 681	21	29.6	4512	22	AAAD16263	Human ATP-binding
c 682	21	29.6	4512	22	AAAD16264	Human ATP-binding
c 683	21	29.6	4795	20	AA332287	M. grisea PTH12 ge
c 684	21	29.6	4843	19	AAV70395	LRP5 isoform 1 cDN
c 685	21	29.6	4896	22	AA159468	Human polynucleoti
c 686	21	29.6	4915	19	AAV70398	LRP5 isoform 3 put
c 687	21	29.6	5021	21	AA246407	Aspergillus oryzae
c 688	21	29.6	5022	19	AAV85549	LRP5 isoform 5 cDN
c 689	21	29.6	5098	19	AAV70396	LRP5 isoform 1 cDN
c 690	21	29.6	5120	22	ABAB2617	Human Zmax1 gene S
c 691	21	29.6	5120	22	ABAB2618	Human HBM gene S5Q
c 692	21	29.6	5125	19	AAV86019	LRP5 isoform 3 cDN
c 693	21	29.6	5263	19	AAV70400	LRP5 isoform 4 cDN
c 694	21	29.6	5438	13	AAQ29263	Human calcium chn
c 695	21	29.6	6114	23	AA559640	Propionibacterium
c 696	21	29.6	6863	21	AACT74847	Human ORFX ORF402
c 697	21	29.6	7286	17	AAAT14547	Cytolactin gene.
c 698	21	29.6	7346	20	AAAT7924	Human tenascin cDN
c 699	21	29.6	7560	22	AAK83437	Human tenascin-C.
c 700	21	29.6	7943	22	AAK83418	Human immune/haema
c 701	21	29.6	8115	22	ABAI6258	Human nervous syst
c 702	21	29.6	8910	23	ABIO3385	Drosophila melanog
c 703	21	29.6	9466	23	ABIO3084	Drosophila melanog
c 704	21	29.6	9733	22	AAAL04203	Human reproductive
c 705	21	29.6	9738	22	AAAL04202	Human reproductive
c 706	21	29.6	14061	23	AAAB03394	Drosophila melanog
c 707	21	29.6	14652	21	AAAB14832	N. meningitidis pa
c 708	21	29.6	15254	22	AAK83335	Human immune/haema
c 709	21	29.6	15254	22	AAK83337	Human immune/haema
c 710	21	29.6	15255	22	AAK83136	Human immune/haema
c 711	21	29.6	15256	22	AAK83134	Human immune/haema
c 712	21	29.6	16499	22	AAK77656	Human immune/haema
c 713	21	29.6	18660	21	AAAS98472	Nucleotide sequenc
c 714	21	29.6	21358	22	AA539919	Genomic sequence #
c 715	21	29.6	21358	22	AAAL06419	Human reproductive
c 716	21	29.6	21358	22	AAK73090	Human immune/haema
c 717	21	29.6	21358	22	AAK87446	Human immune/haema
c 718	21	29.6	21358	22	AAK87558	Human immune/haema
c 719	21	29.6	21358	22	AAK90363	Human immune/haema
c 720	21	29.6	21632	22	AA542019	Human digestive sy
c 721	21	29.6	21676	22	AA539918	Genomic sequence #
c 722	21	29.6	21676	22	AAAL06418	Human reproductive
c 723	21	29.6	21676	22	AAK73081	Human immune/haema
c 724	21	29.6	21676	22	AAK87445	Human immune/haema
c 725	21	29.6	21676	22	AAK87549	Human immune/haema
c 726	21	29.6	21676	22	AAK90362	Human immune/haema
c 727	21	29.6	21948	20	AA520562	Human digestive sy
c 728	21	29.6	27541	23	AAAD17185	Polynucleotide seq
c 729	21	29.6	27541	23	ABLO8332	Streptomyces nous
c 730	21	29.6	30078	21	AAAB1520	Drosophila melanog
c 731	21	29.6	77536	21	AAAI4651	N. meningitidis pa
c 732	21	29.6	107820	22	AAAD16230	Human ATP-binding
c 733	21	29.6	122186	22	AAAC89560	Human histone deac
c 734	21	29.6	125401	22	AAAD17186	Streptomyces nous
c 735	21	29.6	309400	22	AAH68534	C glutamicum codin
c 736	21	29.6	349980	21	AAAF21608	Neisseria meningit
c 737	21	29.6	837096	21	AAAF21611	Neisseria meningit
c 738	21	29.6	837096	21	AAAB1489	N. meningitidis pa
c 739	21	29.6	1437668	21	AAAB1490	N. meningitidis B
c 740	20.8	29.3	740	22	AAU10241	Human breast cance
c 741	20.8	29.3	741	22	AAU19821	Human breast cance
c 742	20.8	29.3	742	22	AAU20499	Human breast cance
c 743	20.8	29.3	743	22	AAH67315	C glutamicum codin
c 744	20.8	29.3	744	22	AAH11601	Human breast cance
c 745	20.8	29.3	745	21	AAAC12042	Human secreted pro
c 746	20.8	29.3	746	19	AAV41442	Nucleotide sequenc
c 747	20.8	29.3	747	324	AAAF98414	5' portion of cDNA
c 748	20.8	29.3	748	22	AAI80095	Human polynucleoti
c 749	20.8	29.3	749	22	AAH66329	EST clone AJ168.
c 750	20.8	29.3	750	22	AAH64514	Novel human polynu
c 751	20.8	29.3	751	22	AAAC0562	Human secreted pro
c 752	20.8	29.3	752	21	AAV42316	Human secreted exp
c 753	20.8	29.3	753	22	AA536173	Human cardiovascular
c 754	20.8	29.3	754	22	AAH80572	Nucleic acid SEQ I
c 755	20.8	29.3	755	22	AAK92939	Human cDNA 3'-end
c 756	20.8	29.3	756	22	AAH67316	C glutamicum codin
c 757	20.8	29.3	757	22	AAK08685	Novel nucleotide s
c 758	20.8	29.3	758	20	AAV01589	Rat neu promoter.
c 759	20.8	29.3	759	22	AAV11431	Human secreted pro
c 760	20.8	29.3	760	22	AAH03566	Human cDNA clone (
c 761	20.8	29.3	761	22	AAH51433	Human UGT1A7 relat
c 762	20.8	29.3	762	22	AAK80289	Human immune/haema
c 763	20.8	29.3	763	22	AAH51432	Human UGT1A7 relat
c 764	20.8	29.3	764	22	AA522493	Human cDNA encodin
c 765	20.8	29.3	765	22	AA522729	Human cDNA encodin
c 766	20.8	29.3	766	22	AAAF94423	Human hydrophobic
c 767	20.8	29.3	767	22	AA593484	DNA encoding novel
c 768	20.8	29.3	768	23	AA593484	Drosophila melanog
c 769	20.8	29.3	769	23	AAH122751	Quorum sensing con
c 770	20.8	29.3	770	23	AAH81355	Sequence of tuf3 g
c 771	20.8	29.3	771	13	AAQ20217	Arabidopsis thalia
c 772	20.8	29.3	772	21	AAAC49878	Arabidopsis thalia
c 773	20.8	29.3	773	22	AAAC33296	Arabidopsis thalia
c 774	20.8	29.3	774	22	AAH44089	Oryza sativa perox
c 775	20.8	29.3	775	22	AAH18288	lung cancer associ
c 776	20.8	29.3	776	15	AAO77979	Nontranslocated el
c 777	20.8	29.3	777	15	AAO77979	Thermophilic alkali
c 778	20.8	29.3	778	18	AAH66463	Porcine BAC-PiGf2-
c 779	20.8	29.3	779	14	AAH66463	3-Hydroxysteroid-o
c 780	20.8	29.3	780	16	AAH85043	3-Hydroxysteroid-o
c 781	20.8	29.3	781	15	AAH85043	Streptomyces sp. s
c 782	20.8	29.3	782	18	AAH62676	Xylanase gene obta
c 783	20.8	29.3	783	22	AAH62676	pseudomonas sp hea
c 784	20.8	29.3	784	22	AAH62676	Human immune/haema
c 785	20.8	29.3	785	22	AAH13768	Human cDNA sequenc
c 786	20.8	29.3	786	16	AAH85042	3-Hydroxysteroid-o
c 787	20.8	29.3	787	16	AAH85042	3-Hydroxysteroid-o
c 788	20.8	29.3	788	19	AAH62675	Streptomyces sp. s
c 789	20.8	29.3	789	17	AAV11823	Human xylose isome
c 790	20.8	29.3	790	24	AAH04219	Hepatitis C virus
c 791	20.8	29.3	791	14	AAH040428	Hepatitis C virus
c 792	20.8	29.3	792	14	AAH040429	Hepatitis C virus
c 793	20.8	29.3	793	14	AAH040430	Hepatitis C virus
c 794	20.8	29.3	794	14	AAH040431	Hepatitis C virus
c 795	20.8	29.3	795	14	AAH040432	Hepatitis C virus
c 796	20.8	29.3	796	14	AAH040433	Hepatitis C virus
c 797	20.8	29.3	797	14	AAH040434	Hepatitis C virus
c 798	20.8	29.3	798	14	AAH040435	Hepatitis C virus
c 799	20.8	29.3	799	14	AAH040436	Hepatitis C virus
c 800	20.8	29.3	800	14	AAH040437	Hepatitis C virus
c 801	20.8	29.3	801	14	AAH040438	Hepatitis C virus
c 802	20.8	29.3	802	14	AAH040439	Hepatitis C virus
c 803	20.8	29.3	803	14	AAH040440	Hepatitis C virus
c 804	20.8	29.3	804	14	AAH040441	Hepatitis C virus
c 805	20.8	29.3	805	14	AAH040442	Hepatitis C virus
c 806	20.8	29.3	806	14	AAH040443	Hepatitis C virus
c 807	20.8	29.3	807	14	AAH040444	Hepatitis C virus
c 808	20.8	29.3	808	14	AAH040445	Hepatitis C virus
c 809	20.8	29.3	809	14	AAH040446	Hepatitis C virus
c 810	20.8	29.3	810	14	AAH040447	Hepatitis C virus
c 811	20.8	29.3	811	14	AAH040448	Hepatitis C virus
c 812	20.8	29.3	812	14	AAH040449	Hepatitis C virus

C 813	20.8	29.3	2341	22	AA158536	Human polynucleotidi
C 814	20.8	29.3	2368	22	AA541588	cDNA encoding nove
C 815	20.8	29.3	2380	22	AAFP94433	Human hydrophobic
C 816	20.8	29.3	2420	21	AAZ46489	PKA substrate, Csk
C 817	20.8	29.3	2429	23	ABLI2674	Drosophila melanog
C 818	20.8	29.3	2466	23	ABLI93804	Human polynucleoti
C 819	20.8	29.3	2488	23	ABLI17627	Drosophila melanog
C 820	20.8	29.3	2496	22	AA523013	DNA encoding novel
C 821	20.8	29.3	2653	21	AAFD0572	Human Hscd6 cDNA.
C 822	20.8	29.3	2694	22	AAFP94452	Human hydrophobic
C 823	20.8	29.3	2732	22	AA508630	Human cDNA (DNA148
C 824	20.8	29.3	2735	22	AA541048	cDNA encoding nove
C 825	20.8	29.3	2774	18	AAAT9535	Human DNA replicat
C 826	20.8	29.3	2777	22	AA508632	Human cDNA (DNA148
C 827	20.8	29.3	3159	21	AA509494	Human DNA encoding
C 828	20.8	29.3	3166	22	AA522919	DNA encoding novel
C 829	20.8	29.3	3202	23	ABLI22750	Drosophila melanog
C 830	20.8	29.3	3400	21	AACT6598	Human ORFX ORF2153
C 831	20.8	29.3	3830	8	AAAT70938	DNA fragment contg
C 832	20.8	29.3	4167	22	ABA08224	Human ovarian and
C 833	20.8	29.3	4167	22	AA529235	Genomic sequence #
C 834	20.8	29.3	4167	22	AA530018	Human lung antigen
C 835	20.8	29.3	4167	22	AAI05022	Human reproductive
C 836	20.8	29.3	4167	22	AAI07543	Human reproductive
C 837	20.8	29.3	4167	22	AA528711	Genomic sequence #
C 838	20.8	29.3	4167	22	AAK68040	Human immune/haema
C 839	20.8	29.3	4167	22	AAK69382	Human digestive sy
C 840	20.8	29.3	4361	22	ABAI9834	Human nervous syst
C 841	20.8	29.3	4445	22	AAI26749	Human breast cance
C 842	20.8	29.3	4454	18	AAAT6462	Plasmid pCRM1.8 co
C 843	20.8	29.3	4708	23	ABLI17626	Drosophila melanog
C 844	20.8	29.3	4808	15	AAO79375	Human N-methyl-D-a
C 845	20.8	29.3	4808	20	AAV82892	Human N-methyl-D-a
C 846	20.8	29.3	4808	21	AA505015	Human N-methyl-D-a
C 847	20.8	29.3	4808	21	AA238706	Human NMDAR2a subu
C 848	20.8	29.3	4808	21	AB199172	Human NMDAR2a enco
C 849	20.8	29.3	5352	22	AAK52403	Human polynucleoti
C 850	20.8	29.3	5948	22	AA506044	Angiotensin conver
C 851	20.8	29.3	6114	21	AA590436	Human GAMP cDNA.
C 852	20.8	29.3	6125	22	AAH72745	Human cervical can
C 853	20.8	29.3	6242	21	AA594955	Human cDNA encodin
C 854	20.8	29.3	7917	23	ABLI18470	Drosophila melanog
C 855	20.8	29.3	8601	24	AB199391	Mouse ischaemic co
C 856	20.8	29.3	9402	14	AAQ41345	Human hepatitis C
C 857	20.8	29.3	9407	23	AA559606	Propionibacterium
C 858	20.8	29.3	11132	22	AAK72302	Human immune/haema
C 859	20.8	29.3	11132	22	AAK72570	Human immune/haema
C 860	20.8	29.3	11200	23	ABLI1695	Drosophila melanog
C 861	20.8	29.3	11293	23	ABAI7918	Human nervous syst
C 862	20.8	29.3	13367	20	AAK20554	Polynucleotide seq
C 863	20.8	29.3	14925	22	AAI03282	Human reproductive
C 864	20.8	29.3	14925	22	AAI04552	Human reproductive
C 865	20.8	29.3	17026	22	AAK70372	Human immune/haema
C 866	20.8	29.3	21747	22	AAK76413	Human immune/haema
C 867	20.8	29.3	21936	22	ABAI5865	Human nervous syst
C 868	20.8	29.3	21936	22	AAI06119	Human reproductive
C 869	20.8	29.3	21936	22	AAI06758	Human reproductive
C 870	20.8	29.3	21936	22	AAI62664	Human breast or ov
C 871	20.8	29.3	22107	22	ABAI7921	Human nervous syst
C 872	20.8	29.3	22107	22	AAK79542	Human immune/haema
C 873	20.8	29.3	22109	22	AAK79543	Human nervous syst
C 874	20.8	29.3	22111	22	ABAI7919	Human immune/haema
C 875	20.8	29.3	22111	22	AAK79540	Human nervous syst
C 876	20.8	29.3	23587	22	AAI07100	Human immune/haema
C 877	20.8	29.3	24028	22	AAI05519	Human reproductive
C 878	20.8	29.3	31659	23	ABLI1694	Human reproductive
C 879	20.8	29.3	31659	23	ABAI08137	Drosophila melanog
C 880	20.8	29.3	31813	22	AAI06997	Human ovarian and
C 881	20.8	29.3	31813	22	ABAI5354	Human reproductive
C 882	20.8	29.3	32134	22	ABAI5813	Human nervous syst
C 883	20.8	29.3	32134	22	AAI04075	Human nervous syst
C 884	20.8	29.3	32134	22	AAI04075	Human reproductive
C 885	20.8	29.3	32191	22	AAI99472	Human excretory re
C 886	20.8	29.3	32191	22	AAI64117	Human bladder rela
C 887	20.8	29.3	32249	22	ABAI1755	Human nervous syst
C 888	20.8	29.3	44840	22	AAK71803	Human immune/haema
C 889	20.8	29.3	75384	22	AAK85590	Human immune/haema
C 890	20.8	29.3	349980	22	AAK85531	C glutamylcystin
C 891	20.6	29.0	182	16	AAAT24875	Human gene signatu
C 892	20.6	29.0	230	21	AAAC02258	Human secreted pro
C 893	20.6	29.0	234	22	AAI26060	Human breast cance
C 894	20.6	29.0	293	22	AAI16858	Human breast cance
C 895	20.6	29.0	493	22	AAH07332	Human cDNA clone (
C 896	20.6	29.0	519	23	AA567274	DNA encoding novel
C 897	20.6	29.0	530	22	AAI195708	Human breast cance
C 898	20.6	29.0	559	21	AAAL1954	Human breast tumou
C 899	20.6	29.0	666	22	AAH48375	Hydrogenase 9 cDNA
C 900	20.6	29.0	738	22	AAH04721	Human cDNA clone (
C 901	20.6	29.0	738	20	AAK86968	Human cDNA clone (
C 902	20.6	29.0	742	22	AAI195708	Human neuroblastom
C 903	20.6	29.0	810	22	AAH01365	Serratia marcescen
C 904	20.6	29.0	840	22	AAH08571	Human cDNA clone (
C 905	20.6	29.0	925	23	AA564421	DNA encoding novel
C 906	20.6	29.0	930	23	AA564422	DNA encoding novel
C 907	20.6	29.0	972	23	ABLI05207	Drosophila melanog
C 908	20.6	29.0	981	23	AA536352	Salmonella typhi D
C 909	20.6	29.0	991	23	ABLI04827	Human polynucleoti
C 910	20.6	29.0	1048	22	AAI58070	Human polynucleoti
C 911	20.6	29.0	1052	22	AAI58070	Human polynucleoti
C 912	20.6	29.0	1161	24	AAAD21925	M. rosaria PMR2 pl
C 913	20.6	29.0	1172	23	ABLI2997	Drosophila melanog
C 914	20.6	29.0	1289	16	AAQ09001	Bovine herpes viru
C 915	20.6	29.0	1332	23	AA579247	DNA encoding novel
C 916	20.6	29.0	1332	23	AA585618	DNA encoding novel
C 917	20.6	29.0	1332	23	AA589467	DNA encoding novel
C 918	20.6	29.0	1379	21	AACT7752	Human cancer assoc
C 919	20.6	29.0	1400	21	AAAC62024	Nucleotide sequenc
C 920	20.6	29.0	1401	21	AACT77259	Human ORFX ORF2814
C 921	20.6	29.0	1424	22	AAH15200	Human cDNA sequenc
C 922	20.6	29.0	1500	22	AAAD05515	Human secreted pro
C 923	20.6	29.0	1602	22	AAH18715	Human cDNA sequenc
C 924	20.6	29.0	1736	17	AAAT37149	5' end of chicken
C 925	20.6	29.0	1791	23	ABLI2413	Drosophila melanog
C 926	20.6	29.0	1821	16	AAQ09366	S. lividans protea
C 927	20.6	29.0	1821	20	AAV84068	Clone p5-6 encodin
C 928	20.6	29.0	1821	21	AAAC61406	cDNA encoding a su
C 929	20.6	29.0	1823	22	AAK51475	Human polynucleoti
C 930	20.6	29.0	1827	22	AAAF61092	P. putida KT2440-a
C 931	20.6	29.0	1852	22	AAH18681	Human cDNA sequenc
C 932	20.6	29.0	1899	24	AAI67923	Human LGR6 polyep
C 933	20.6	29.0	1905	23	ABLI12412	Drosophila melanog
C 934	20.6	29.0	1926	23	AAV82522	Sphingomonas capsu
C 935	20.6	29.0	2066	23	AA579668	DNA encoding novel
C 936	20.6	29.0	2087	22	AA558866	Rat Glutyl coding
C 937	20.6	29.0	2122	23	AA584647	DNA encoding novel
C 938	20.6	29.0	2131	22	AAAD05492	Human secreted pro
C 939	20.6	29.0	2455	22	AAH16124	Human cDNA sequenc
C 940	20.6	29.0	2485	22	AAH14775	Human LGR6 polyep
C 941	20.6	29.0	2486	24	AAI67922	Human cDNA sequenc
C 942	20.6	29.0	2488	22	AAH17665	Human cDNA sequenc
C 943	20.6	29.0	2507	22	AAAC86398	SHEXN DNA #2. Hom
C 944	20.6	29.0	2637	22	AA528378	Human cDNA encodin
C 945	20.6	29.0	2681	23	AA584829	Thermophilus therm
C 946	20.6	29.0	2681	23	ABLI05206	Drosophila melanog
C 947	20.6	29.0	2695	23	ABLI23195	Drosophila melanog
C 948	20.6	29.0	2727	23	AA554113	Pseudomonas aerugi
C 949	20.6	29.0	2742	19	AAV33481	Pseudomonas Orfx s
C 950	20.6	29.0	2742	21	AAAI3898	Pseudomonas alcali
C 951	20.6	29.0	2742	24	AAAD2875	Pseudomonas alcali
C 952	20.6	29.0	2838	22	AAAF61007	P. putida KT2440-a
C 953	20.6	29.0	2856	23	AA56118	Salmonella typhi D
C 954	20.6	29.0	2991	23	ABLI04826	Drosophila melanog
C 955	20.6	29.0	3000	20	AA584399	S. capsulata fROI2
C 956	20.6	29.0	3003	19	AAV19375	Hereditary multipl
C 957	20.6	29.0	3013	23	AAV01451	Plasmid pANT195 in
C 958	20.6	29.0	3022	19	ABLI3806	Drosophila melanog

959	20.6	29.0	3045	23	ABL21316	Drosophila melanog
960	20.6	29.0	3175	20	AA08224	Human Ext-2 cDNA.
961	20.6	29.0	3179	22	AAH33311	Human colon cancer
962	20.6	29.0	3311	18	AAT70377	Cytoshesin 1. Homo
963	20.6	29.0	3543	23	ABL16717	Drosophila melanog
964	20.6	29.0	3572	19	AAV67162	Drosophila kinesin
965	20.6	29.0	3610	20	ABL12996	Drosophila melanog
966	20.6	29.0	3691	23	AAV59404	Human matrix-type
967	20.6	29.0	3713	23	ABL10425	Drosophila melanog
968	20.6	29.0	3720	23	ABL13337	Drosophila melanog
969	20.6	29.0	3783	23	ABL06641	Drosophila melanog
970	20.6	29.0	3789	13	AA030183	Bovine brain clone
971	20.6	29.0	3798	19	AAV06533	Mouse SCA2 cDNA en
972	20.6	29.0	4057	23	ABL19624	Drosophila melanog
973	20.6	29.0	4418	22	AAK77953	Human immune/haema
974	20.6	29.0	4431	22	AAK77956	Human immune/haema
975	20.6	29.0	4456	23	ABL16125	Drosophila melanog
976	20.6	29.0	4614	23	ABL14340	Drosophila melanog
977	20.6	29.0	4636	21	AA65530	Porcine BAC-PIGF2-
978	20.6	29.0	4848	24	AA022684	Streptomyces fradi
979	20.6	29.0	4936	22	AA07030	Alcaligenes latus
980	20.6	29.0	4936	22	AA07030	Human reproductive
981	20.6	29.0	5870	22	AA07069	Human immune/haema
982	20.6	29.0	5870	22	AA084149	Human ORFX ORF2601
983	20.6	29.0	6104	21	AA077046	Human immune/haema
984	20.6	29.0	6181	22	AAK77952	Human immune/haema
985	20.6	29.0	6192	23	ABL19622	Drosophila melanog
986	20.6	29.0	6195	22	AAK77956	Human immune/haema
987	20.6	29.0	6225	23	ABL10424	Drosophila melanog
988	20.6	29.0	6228	23	ABL06640	Drosophila melanog
989	20.6	29.0	6313	23	ABL23194	Drosophila melanog
990	20.6	29.0	6436	20	AA086965	DNA containing PHA
991	20.6	29.0	6640	23	ABL16124	Drosophila melanog
992	20.6	29.0	6854	19	AAT76903	S. glaucescens pst
993	20.6	29.0	7014	23	ABL13336	Drosophila melanog
994	20.6	29.0	7078	22	ABL03681	Drosophila melanog
995	20.6	29.0	7120	22	ABAI4810	Human nervous syst
996	20.6	29.0	9320	22	AAH45588	Human encoding hydro
997	20.6	29.0	9390	19	AAT76929	GT230 genomic RNA
998	20.6	29.0	9390	19	AAT76931	GT230 gene cDNA se
999	20.6	29.0	11188	24	AA021912	Micromonospora ros
c1000	20.6	29.0	12468	22	AA067330	Human Immune/haema

ALIGNMENTS

RESULT 1
 ID AA089226 standard; cDNA; 1610 BP.
 AC AA089226;
 XX
 DT 20-OCT-1995 (first entry)
 XX
 DE Human mu opioid receptor cDNA.
 XX
 KM Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 239..1441
 FT /*tag= a
 XX
 PN W09507983-A.
 XX
 PD 23-MAR-1995.
 XX
 PF 13-SEP-1994; 94MO-US10358.
 XX
 PR 13-SEP-1993; 93US-0120601.
 XX

PA (INDV) UNIV INDIANA FOUND.
 PI Yu L;
 XX
 DR WPI: 1995-131351/17.
 DR P-PSDB; AAR71966.
 XX
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Claim 5; Page 208-210; 266pp; English.
 XX
 CC A cDNA library constructed from human caudate nucleus mRNA was
 CC screened with rat mu opioid receptor cDNA under conditions of
 CC low stringency. One positive clone included the sequence given in
 CC AA089226, encoding a mu opioid receptor MOR (AAR71964). The cDNA
 CC is used for prodn. of recombinant MOR, in gene therapy, etc.
 XX
 SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;
 Query Match 100.0%; Score 71; DB 16; Length 1610;
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCTGTCGACCCATGCGGTCCGACCGACCGACCTGGCGGAGAGACGCTGT 60
 Db 354 GCACCTGTCGACCCATGCGGTCCGACCGACCGACCGACCTGGCGGAGAGACGCTGT 413
 QY 61 GCCCTCGACC 71
 Db 414 GCCCTCGACC 424
 RESULT 2
 ID AA059503 standard; cDNA; 1610 BP.
 AC AA059503;
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE cDNA encoding a human mu opioid receptor polypeptide.
 XX
 KM mu opioid receptor; transcription regulatory polypeptide;
 KM opioid receptor-like polypeptide; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 239..1441
 FT /*tag= a
 FT /product= "mu opioid receptor"
 XX
 PN US6103492-A.
 XX
 PD 15-AUG-2000.
 XX
 PF 07-JUL-1997; 97US-0889108.
 XX
 PR 13-SEP-1994; 94US-030518.
 PR 08-MAR-1993; 93US-0056886.
 PR 13-SEP-1993; 93US-0120601.
 XX
 PA (INDV) UNIV INDIANA.
 XX
 PI Yu L;
 XX
 DR WPI: 2000-542550/49.
 DR P-PSDB; AAB07866.
 XX
 PT Novel nucleic acids encoding mu opioid receptor for expressing large
 PT quantities opioid receptors which are useful for screening and

PT evaluating subtype-selective drugs and as probes or primers -
XX
PS Claim 17; Column 99-102; 86pp; English.
XX
CC The present sequence encodes a mu opioid receptor protein. The
CC specification also describes a transcription regulatory polypeptide
CC and an opioid receptor-like polypeptide. Human mu opioid receptor
CC polynucleotides are useful as a source of probes and primers, which
CC may be used as diagnostic tools to detect normal and abnormal DNA
CC sequences in DNA derived from patients cells. They are also used as
CC a means for detecting and isolating other members of the polypeptide
CC family and related polypeptides from a DNA library potentially
CC containing such sequences. The polynucleotide is used for preparing
CC large quantities of opioid receptor which on expression in
CC microorganism can be useful for evaluating subtype-selective drugs.
XX
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 100.0%; Score 71; DB 21; Length 1610;
Best Local Similarity 100.0%; Pred. No. 11e-13;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCTGTCGACCCATGCGGTCCGAACCGCACCTGGCGGAGAGACACCTGT 60
DB 354 GCACCTGTCGACCCATGCGGTCCGAACCGCACCTGGCGGAGAGACACCTGT 413
QY 61 GCCCTCCGACC 71
DB 414 GCCCTCCGACC 424

RESULT 3
ABI98013
ID ABI98013 standard; cDNA; 1182 BP.
XX
AC ABI98013;
XX
DT 18-FEB-2002 (first entry)
XX
DE Non-endogenous human GPCR cDNA, SEQ ID NO: 546.
XX
KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PE 05-APR-2001; 2001WO-US11098.
XX
PR 07-APR-2000; 2000US-195747P.
XX
PS (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI: 2001-648759/74.
DR P-PSDB; ABB56377.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX
PS Example 2; Page 347-348; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such

CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence encodes a non-endogenous
CC version of a known human GPCR.
XX
SQ Sequence 1182 BP; 292 A; 343 C; 241 G; 306 T; 0 other;

Query Match 97.7%; Score 69.4; DB 23; Length 1182;
Best Local Similarity 98.6%; Pred. No. 3.3e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACCTGTCGACCCATGCGGTCCGAACCGCACCTGGCGGAGAGACACCTGT 60
DB 116 GCACCTGTCGACCCATGCGGTCCGAACCGCACCTGGCGGAGAGACACCTGT 175
QY 61 GCCCTCCGACC 71
DB 176 GCCCTCCGACC 186

RESULT 4
ABI98012
ID ABI98012 standard; cDNA; 1203 BP.
XX
AC ABI98012;
XX
DT 18-FEB-2002 (first entry)
XX
DE Non-endogenous human GPCR cDNA, SEQ ID NO: 544.
XX
KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PE 05-APR-2001; 2001WO-US11098.
XX
PR 07-APR-2000; 2000US-195747P.
XX
PS (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI: 2001-648759/74.
DR P-PSDB; ABB56376.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX
PS Example 2; Page 345-346; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence encodes a non-endogenous
CC version of a known human GPCR.
XX
SQ Sequence 1203 BP; 301 A; 348 C; 245 G; 309 T; 0 other;

Query Match 97.7%; Score 69.4; DB 23; Length 1203;
Best Local Similarity 98.6%; Pred. No. 3.3e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCACCTGTCGACCCATGCGGTCCGAACCGCACCTGGCGGAGAGACACCTGT 60
|||||

```

Db      116 GCAACCTGTCGACCCATGCGGTCCGACCGACCAACTGGCGGAGAGACGCTGT 175
OY      61 GCCCTCCGACC 71
        |||||||
Db      176 GCCCTCCGACC 186

RESULT 5
AA093102
ID      AA093102 standard: cDNA; 2160 BP.
XX
XX      AA093102:
XX
XX      11-DEC-1995 (first entry)
XX
XX      Human mu opiate receptor cDNA.
XX
XX      Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
XX      drug abuse; analgesic; ds.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      213..1415
                /*tag= a
XX
XX      WO9520667-A1.
XX
XX      03-AUG-1995.
XX
XX      30-JAN-1995; 95WO-US01144.
XX
XX      28-JAN-1994; 94US-0188275.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX      (USSH ) US SEC DEPT HEALTH.
XX
XX      Johnson PS, Persico AM, Uhl G, Wang J;
XX
XX      MPI; 1995-275452/36.
XX      P-PSDB; AAR76780.
XX
XX      New DNA encoding human mu opiate receptor - used esp. for screening
XX      cpds. for activity as opiate agonists or antagonists
XX
XX      Claim 4: Page 24-25; 49pp; English.
XX
XX      hMOR cDNA was obtd. from a human cerebral cortical cDNA library
XX      screened with fragments of a rat mu opiate receptor. Cloned hMOR
XX      cDNA can be used as probes to examine the structure and function of
XX      hMOR genes or to screen individuals for susceptibility to drug
XX      abuse. Expression in e.g. COS cells allows production of
XX      recombinant hMOR1.
XX
XX      Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T; 0 other:
SQ
Query Match      97.7%; Score 69.4; DB 16; Length 2160;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 GCACCTGTCGACCCATGCGGTCCGACCGACCAACTGGCGGAGAGACGCTGT 60
        |||||||
Db      328 GCAACCTGTCGACCCATGCGGTCCGACCGACCAACTGGCGGAGAGACGCTGT 387
OY      61 GCCCTCCGACC 71
        |||||||
Db      388 GCCCTCCGACC 398

RESULT 6
AAV61985
ID      AAV61985 standard: cDNA; 2162 BP.
XX

```

```

AC      AAV61985;
XX
XX      11-JAN-1999 (first entry)
XX
XX      Human mu-opioid receptor cDNA variant 1.
XX
XX      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX      predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX      psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX      cocaine; inherited alcoholism; human; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      CDS      213..2040
                /*tag= a
                /product= "mu-opioid receptor"
                /note= b
                /*tag= b
                /note= "Site of intron 1"
                855..856
                /*tag= c
                /note= "Site of intron 2"
                1376..1377
                /*tag= d
                /note= "Site of intron 3"
                41
                /*tag= e
                /note= "Wild type G is replaced by T"
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE00382.
XX
XX      03-FEB-1997; 97DE-1003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      MPI; 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
XX      used, e.g. to predict pre-disposition to addiction and for
XX      development of analgesics, anaesthetics and anti-addiction agents
XX
XX      Claim 8: Page -; 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a G
XX      nucleotide at position 41 of the wild-type sequence represented in
XX      AAV61984 is replaced by a T. The wild type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predisposition to disease, particularly addictive disease, by isolating
XX      cDNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic,
XX      anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX      genes and vectors, particularly for pharmaceutical development, to
XX      develop diagnostic kits for predicting risk of addiction, response to
XX      analgesics or anaesthetics, or development of side effects from a drug.
XX      Particular applications are, or development of side effects from a drug.
XX      cocaine, or of developing inherited alcoholism.
XX      Note: This sequence is not represented in the specification and has
XX      been constructed from the wild-type sequence represented in AAV61984 in
XX      accordance with the specification.
XX
XX      Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 2 other:
SQ
Query Match      97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 GCAACCTGTCGACCATCGGTCCGACCGACCGACCTGGCGGAGAGACAGCCTGT 60
 |||
 DB 328 GCAACCTGTCGACCATCGGTCCGACCGACCGACCACTGGCGGAGAGACAGCCTGT 387
 |||
 QY 61 GCCCTCCGACC 71
 |||
 DB 388 GCCCTCCGACC 398
 |||

RESULT 7
 AAV61984
 ID AAV61984 standard; cDNA; 2162 BP.
 XX AAV61984;
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA.
 XX
 KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KM prediosition; addiction; analgesic; anaesthetic; anti-addictive;
 KM psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KM cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..2040
 FT /*tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /*tag= b
 FT /note= "Site of intron 1"
 FT misc_feature 855..856
 FT /*tag= c
 FT /note= "Site of intron 2"
 FT misc_feature 1376..1377
 FT /*tag= d
 FT /note= "Site of intron 3"
 FT
 XX
 PN WO9833937-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Hoehe M, Wendel B;
 XX
 DR WPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page 14-15; 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor. This sequence and
 CC its variants, polymorphisms and mutants are used in a method for
 CC detecting prediosition to disease, particularly addictive disease, by
 CC isolating DNA from a sample, genotyping selected positions and comparing
 CC with a reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism.
 XX

SQ Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 2 other;
 Query Match 97.7%; Score 69.4; DB 19; Length 2162;
 Best Local Similarity 98.6%; Pred. No. 3.5e-13;
 Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCCGACCGACCGACCTGGCGGAGAGACAGCCTGT 60
 |||
 DB 328 GCAACCTGTCGACCATCGGTCCGACCGACCGACCACTGGCGGAGAGACAGCCTGT 387
 |||
 QY 61 GCCCTCCGACC 71
 |||
 DB 388 GCCCTCCGACC 398
 |||

RESULT 8
 AAV61986
 ID AAV61986 standard; cDNA; 2162 BP.
 XX AAV61986;
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 2.
 XX
 KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KM prediosition; addiction; analgesic; anaesthetic; anti-addictive;
 KM psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KM cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..2040
 FT /*tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /*tag= b
 FT /note= "Site of intron 1"
 FT misc_feature 855..856
 FT /*tag= c
 FT /note= "Site of intron 2"
 FT misc_feature 1376..1377
 FT /*tag= d
 FT /note= "Site of intron 3"
 FT mutation 80
 FT /*tag= e
 FT /note= "Wild type C is replaced by T"
 FT
 XX
 PN WO9833937-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Hoehe M, Wendel B;
 XX
 DR WPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -; 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which a C
 CC nucleotide at position 80 of the wild-type sequence represented in
 CC AAV61984 is replaced by a T. The wild type receptor and its variants,
 XX

CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmacological agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;
Query Match 97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAACCTGTCGACCCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 60
|||||
Db 328 GCAACCTGTCGACCCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 387
QY 61 GCCCTCCGACC 71
|||||
Db 388 GCCCTCCGACC 398
RESULT 9
AAV61987
ID AAV61987 standard; cDNA; 2162 BP.
XX
AC AAV61987;
XX
DT 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 3.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /*tag- a
FT FT /product= "mu-opioid receptor"
FT FT 502..503
FT FT /*tag- b
FT FT /note= "Site of intron 1"
FT FT 855..856
FT FT /*tag- c
FT FT /note= "Site of intron 2"
FT FT 1376..1377
FT FT /*tag- d
FT FT /note= "Site of intron 3"
FT FT 102
FT FT mutation
FT FT /*tag- e
FT FT /note= "Wild type C is replaced by T"
XX
XX PN W09833937-A2.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-DE00382.
XX
XX 03-FEB-1997; 97DE-1003925.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX
PI Hoehe M, Wendel B;
XX
DR WPL; 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 102 of the wild-type sequence represented in
CC AAV61984 is replaced by a T. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmacological agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;
Query Match 97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAACCTGTCGACCCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 60
|||||
Db 328 GCAACCTGTCGACCCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT 387
QY 61 GCCCTCCGACC 71
|||||
Db 388 GCCCTCCGACC 398
RESULT 10
AAV61988
ID AAV61988 standard; cDNA; 2162 BP.
XX
AC AAV61988;
XX
DT 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 4.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /*tag- a
FT FT /product= "mu-opioid receptor"
FT FT 502..503
FT FT /*tag- b
FT FT /note= "Site of intron 1"
FT FT 855..856
FT FT /*tag- c
FT FT /note= "Site of intron 2"
FT FT 1376..1377
FT FT /*tag- d
FT FT misc-feature

```

FT      /note= "Site of intron 3"
FT      175
FT      mutation
FT      /tag= e
FT      /note= "Wild type C is replaced by A"
XX
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE00382.
XX
XX      03-FEB-1997; 97DE-1003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      WPI: 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
XX      used, e.g. to predict pre-disposition to addiction and for
XX      development of analgesics, anaesthetics and anti-addiction agents
XX
XX      Claim 8: Page -: 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
XX      nucleotide at position 175 of the wild-type sequence represented in
XX      AAV61984 is replaced by an A. The wild type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predisposition to disease, particularly addictive disease, by isolating
XX      DNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic,
XX      anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX      genes and vectors, particularly for pharmaceutical development, to
XX      develop diagnostic kits for predicting risk of addiction, response to
XX      analgesics or anaesthetics, or development of side effects from a drug.
XX      Particular applications are to determine risk of addiction to opiates or
XX      cocaine, or of developing inherited alcoholism.
XX      Note: This sequence is not represented in the specification and has
XX      been constructed from the wild-type sequence represented in AAV61984 in
XX      accordance with the specification.
XX
XX      Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:
XX
XX      Query Match          97.7%; Score 69.4; DB 19; Length 2162;
XX      Best Local Similarity 98.6%; Pred. No. 3.5e-13;
XX      Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      1 GCACCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGCGGAGAGACAGCCTGT 60
XX      GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
XX      DB 328 GCAACCTGTCCGACCATCGGTCCGACCGACCGACCACTGGGGGAGAGACAGCCTGT 387
XX
XX      61 GCCCTCCGACC 71
XX      |||||||
XX      DB 388 GCCCTCCGACC 398
XX
XX      RESULT 11
XX      AAV61989
XX      ID AAV61989 standard; cDNA: 2162 BP.
XX
XX      AAV61989;
XX
XX      11-JAN-1999 (first entry)
XX
XX      Human mu-opioid receptor cDNA variant 5.
XX
XX      Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX      predisposition; addiction; analgesic; anaesthetic; anti-addictive;
XX      psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX      cocaine; inherited alcoholism; human; ss.
XX
XX      Homo sapiens.

```

```

OS      Synthetic.
XX
XX      Key
XX      CDS
XX
XX      Location/Qualifiers
XX      213..2040
XX      /tag= a
XX      /product= "mu-opioid receptor"
XX      502..503
XX      /tag= b
XX      /note= "Site of intron 1"
XX      855..856
XX      /tag= c
XX      /note= "Site of intron 2"
XX      1376..1377
XX      /tag= d
XX      /note= "Site of intron 3"
XX      229
XX      /tag= e
XX      /note= "Wild type C is replaced by T"
XX
XX      WO9833937-A2.
XX
XX      06-AUG-1998.
XX
XX      02-FEB-1998; 98WO-DE00382.
XX
XX      03-FEB-1997; 97DE-1003925.
XX
XX      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX      Hoehe M, Wendel B;
XX
XX      WPI: 1998-437487/37.
XX
XX      New genomic and cDNA sequences encoding human mu-opioid receptor -
XX      used, e.g. to predict pre-disposition to addiction and for
XX      development of analgesics, anaesthetics and anti-addiction agents
XX
XX      Claim 8: Page -: 26pp; German.
XX
XX      This sequence encodes a novel human mu-opioid receptor in which a C
XX      nucleotide at position 229 of the wild-type sequence represented in
XX      AAV61984 is replaced by an T. The wild type receptor and its variants,
XX      polymorphisms and mutants are used in a method for detecting
XX      predisposition to disease, particularly addictive disease, by isolating
XX      DNA from a sample, genotyping selected positions and comparing with a
XX      reference DNA. Such sequences are used to develop analgesic,
XX      anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX      genes and vectors, particularly for pharmaceutical development, to
XX      develop diagnostic kits for predicting risk of addiction, response to
XX      analgesics or anaesthetics, or development of side effects from a drug.
XX      Particular applications are to determine risk of addiction to opiates or
XX      cocaine, or of developing inherited alcoholism.
XX      Note: This sequence is not represented in the specification and has
XX      been constructed from the wild-type sequence represented in AAV61984 in
XX      accordance with the specification.
XX
XX      Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other:
XX
XX      Query Match          97.7%; Score 69.4; DB 19; Length 2162;
XX      Best Local Similarity 98.6%; Pred. No. 3.5e-13;
XX      Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      1 GCACCTGTCCGACCATCGGTCCGACCGACCGACCTGGGGCGGAGAGACAGCCTGT 60
XX      GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
XX      DB 328 GCAACCTGTCCGACCATCGGTCCGACCGACCGACCAACTGGGGGAGAGACAGCCTGT 387
XX
XX      61 GCCCTCCGACC 71
XX      |||||||
XX      DB 388 GCCCTCCGACC 398
XX
XX      RESULT 12
XX      AAV61991

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ID AAV61991 standard; cDNA; 2162 BP.
XX
AC AAV61991;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 7.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predispotion; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /tag= a
FT FT /product= "mu-opioid receptor"
FT FT 502..503
FT FT /tag= b
FT FT /note= "Site of intron 1"
FT FT 855..856
FT FT /tag= c
FT FT /note= "Site of intron 2"
FT FT 1376..1377
FT FT /tag= d
FT FT /note= "Site of intron 3"
FT FT 666
FT FT /tag= e
FT FT /note= "Wild type A is replaced by G"
XX
PN W09833937-A2.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-DE00382.
XX
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
DR WPI; 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which an A
CC nucleotide at position 666 of the wild-type sequence represented in
CC AAV61984 is replaced by a G. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predispotion to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;
Query Match 97.7%; Score 69.4; DB 19; Length 2162;

Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCACCTGTCGACCGCATGCGGTCGAAACCGACGACGCGGAGACAGCCTGT 60
DB 328 GCACCTGTCGACCGCATGCGGTCGAAACCGACGACGCGGAGACAGCCTGT 387
QY 61 GCCCTCCGACC 71
DB 388 GCCCTCCGACC 398
RESULT 13
ID AAV61992 standard; cDNA; 2162 BP.
XX
AC AAV61992;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 8.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predispotion; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /tag= a
FT FT /product= "mu-opioid receptor"
FT FT 502..503
FT FT /tag= b
FT FT /note= "Site of intron 1"
FT FT 855..856
FT FT /tag= c
FT FT /note= "Site of intron 2"
FT FT 1376..1377
FT FT /tag= d
FT FT /note= "Site of intron 3"
FT FT 1006
FT FT /tag= e
FT FT /note= "Wild type G is replaced by A"
XX
PN W09833937-A2.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-DE00382.
XX
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
DR WPI; 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1006 of the wild-type sequence represented in
CC AAV61984 is replaced by an A. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predispotion to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a

CC reference DNA. Such sequences are used to develop analgesic,
CC anesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other:
Query Match 97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATCGGTCCGAAACCGACCGACCTGGCGGAGAGACAGCTGT 60
DB 328 GCAACCTGTCCGACCCATCGGTCCGAAACCGACCGACCTGGCGGAGAGACAGCTGT 387
OY 61 GCCCTCCGACC 71
DB 388 GCCCTCCGACC 398
RESULT 14
AAV61993
ID AAV61993 standard; cDNA: 2162 BP.
XX
AC AAV61993;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 9.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT /tag= a
FT /product= "mu-opioid receptor"
FT /tag= b
FT /note= "Site of intron 1"
FT 855..856
FT /tag= c
FT /note= "Site of intron 2"
FT 1376..1377
FT /tag= d
FT /note= "Site of intron 3"
FT 1014
FT /tag= e
FT /note= "Wild type T is replaced by C"
XX
XX MO9833937-A2.
XX
XX PD 06-AUG-1998.
XX
XX PF 02-FEB-1998; 98WO-DE00382.
XX
XX PR 03-FEB-1997; 97DE-1003925.
XX
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX PI Hoehe M, Wendel B;
XX

DR WPI; 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
PS
PS Claim 8: Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a T
CC nucleotide at position 1014 of the wild-type sequence represented in
CC AAV61984 is replaced by a C. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly additive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 2 other:
Query Match 97.7%; Score 69.4; DB 19; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATCGGTCCGAAACCGACCGACCTGGCGGAGAGACAGCTGT 60
DB 328 GCAACCTGTCCGACCCATCGGTCCGAAACCGACCGACCTGGCGGAGAGACAGCTGT 387
OY 61 GCCCTCCGACC 71
DB 388 GCCCTCCGACC 398
RESULT 15
AAV61994
ID AAV61994 standard; cDNA: 2162 BP.
XX
AC AAV61994;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 10.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT /tag= a
FT /product= "mu-opioid receptor"
FT /tag= b
FT /note= "Site of intron 1"
FT 855..856
FT /tag= c
FT /note= "Site of intron 2"
FT 1376..1377
FT /tag= d
FT /note= "Site of intron 3"
FT 1154
FT /tag= e
XX
XX mutation
XX

/note= "Wild type G is replaced by A"

FT XX WO9833937-A2.
 XX PN 06-AUG-1998.
 XX PD
 XX PF 02-FEB-1998; 98WO-DE00382.
 XX PR 03-FEB-1997; 97DE-1003925.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Hoehe M, Wendel B;
 XX DR WPI; 1998-437487/37.
 XX PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX PS Claim 8; Page -: 26pp; German.
 XX CC This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 1154 of the wild-type sequence represented in
 CC AAV61984 is replaced by an A. The wild-type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in AAV61984 in
 CC accordance with the specification.
 CC XX
 SQ Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other;
 CC
 Query Match 97.7%; Score 69.4; DB 19; Length 2162;
 Best Local Similarity 98.6%; Pred. No. 3.5e-13;
 Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACTGTCTCGAAGCCATGCGTCCGAACCGCAGCTGGCGGAGAGACAGCCTGT 60
 DB 328 GCAACTGTCTCGAAGCCATGCGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 387
 QY 61 GCCCTCGACC 71
 DB 388 GCCCTCGACC 398

RESULT 16
 AAV61995
 ID AAV61995 standard; cDNA; 2162 BP.
 XX
 AC AAV61995;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 11.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH key Location/Qualifiers

FT CDS 213..2040
 FT /tag- a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /tag- b
 FT /note= "Site of intron 1"
 FT misc_feature 855..856
 FT /tag- c
 FT /note= "Site of intron 2"
 FT misc_feature 1376..1377
 FT /tag- d
 FT /note= "Site of intron 3"
 FT mutation 1613
 FT /tag- e
 FT /note= "Wild type G is replaced by C"
 FT XX
 XX PN WO9833937-A2.
 XX PD 06-AUG-1998.
 XX PF 02-FEB-1998; 98WO-DE00382.
 XX PR 03-FEB-1997; 97DE-1003925.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Hoehe M, Wendel B;
 XX DR WPI; 1998-437487/37.
 XX PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX PS Claim 8; Page -: 26pp; German.
 XX CC This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 1613 of the wild-type sequence represented in
 CC AAV61984 is replaced by a C. The wild-type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic,
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
 CC genes and vectors, particularly for pharmaceutical development, to
 CC develop diagnostic kits for predicting risk of addiction, response to
 CC analgesics or anaesthetics, or development of side effects from a drug.
 CC Particular applications are to determine risk of addiction to opiates or
 CC cocaine, or of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in AAV61984 in
 CC accordance with the specification.
 CC XX
 SQ Sequence 2162 BP; 562 A; 566 C; 457 G; 575 T; 2 other;
 CC
 Query Match 97.7%; Score 69.4; DB 19; Length 2162;
 Best Local Similarity 98.6%; Pred. No. 3.5e-13;
 Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAACTGTCTCGAAGCCATGCGTCCGAACCGCAGCTGGCGGAGAGACAGCCTGT 60
 DB 328 GCAACTGTCTCGAAGCCATGCGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 387
 QY 61 GCCCTCGACC 71
 DB 388 GCCCTCGACC 398

RESULT 17
 AAZ88470
 ID AAZ88470 standard; DNA; 2162 BP.
 XX
 AC AAZ88470;

XX 11-MAY-2000 (first entry)
DT Human mu opioid receptor gene.
XX
DE
XX Human; mu opioid receptor; hMOR1; diagnosis; addiction; constipation;
KW diarrhoea; decreased immune response; stress; gastrointestinal motility;
KW immune response; hypothalamus pituitary adrenal axis; gonadal axis;
KW pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;
KW anxiolytic; alcohol; ds.
XX
OS Homo sapiens.
XX
PN WO200003024-A2.
XX
PD 20-JAN-2000.
XX
PF 10-JUL-1999; 99WO-US15707.
XX
PR 10-JUL-1998; 98US-0113426.
PR 09-JUL-1999; 99US-0113426.
XX
PA (UTRQ) UNIV ROCKEFELLER.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
PI Kreek MJ, LaForge KS, Yu L, Tischfield JA;
XX
DR WPI: 2000-160930/14.
DR P-PSDB: AAV79945.
XX
PT New human opioid mu receptor gene variant for determining
PT susceptibility of a subject to addictive disorder, pain -
XX
PS Claim 1; Page -: 134pp: English.
XX
XX The present invention describes an isolated variant (V) of the human
CC mu opioid receptor (hMOR1) gene with at least two variations A118G,
CC C17T, G24A, G779A or G942A of the sequence of Genbank accession number
CC L25119. Determination of increased or decreased susceptibility in a
CC subject to at least one addictive disorder like opioid, cocaine,
CC nicotine, barbiturate or sedative hypnotic, anxiolytic, alcohol
CC addition or addiction to others psychostimulants and to pain is done
CC by determining the presence of (V) with variation A118G or C17T
CC respectively in one and/or both alleles of (V) and it can also be done
CC by determining the presence of the hMOR1 protein with variation Asn40Asp
CC or Ala6Val respectively. Therapeutically effective amount of pain
CC reliever to induce analgesia or therapeutic agent to treat one additive
CC disorder is determined by determining the variations in the hMOR1 gene
CC or protein and so increased or decreased susceptibility indicates an
CC increased or decreased amount of pain reliever or therapeutic agent
CC respectively. The determination of the hMOR1 gene with variation A118G
CC or C17T also helps in the diagnosis of a disease or disorder like
CC infertility constipation, diarrhoea, decreased immune response or
CC decreased ability to withstand stress related to physiological function
CC like sexual or reproductive function, gastrointestinal motility, immune
CC response, or ability to withstand stress regulated by hypothalamus
CC pituitary adrenal axis (HPA) or gonadal axis (HPG). The present sequence
CC represents the hMOR1 gene.
CC N.B. The present sequence is not given in the present invention but
CC is referred to as the Genbank accession number L25119.
XX
SQ Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 2 other;

Query Match 97.7%; Score 69.4; DB 21; Length 2162;
Best Local Similarity 98.6%; Pred. No. 3.5e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCAACCTGCGAGCCATGCGGTCGACCGACCGACTGGCGGAGAGACAGCCTGT 60
Db 328 GCAACCTGCGAGCCATGCGGTCGACCGACCGACTGGCGGAGAGACAGCCTGT 387
OY 61 GCGCTCGGACC 71
|||||

Db 388 GCGCTCGGACC 398
RESULT 18
AAV61990
ID AAV61990 standard; cDNA: 2162 BP.
XX
AC AAV61990;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 6.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT misc_feature 502..503
FT /tag= b
FT /note= "Site of intron 1"
FT misc_feature 855..856
FT /tag= c
FT /note= "Site of intron 2"
FT misc_feature 1376..1377
FT /tag= d
FT /note= "Site of intron 3"
FT mutation 330
FT /tag= e
FT /note= "Wild type A is replaced by G"
XX
PN WO9833937-A2.
XX
PD 06-AUG-1998.
XX
PR 02-FEB-1998; 98WO-DE00382.
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
DR WPI: 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
CC nucleotide at position 330 of the wild-type sequence represented in
CC AAV61984 is replaced by a G. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anaesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in

CC accordance with the specification.
XX
SQ Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other:
Query Match 95.5%; Score 67.8; DB 19; Length 2162;
Best Local Similarity 97.2%; Pred. No. 1.1e-12;
Matches 69; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GCAACCTGTCGACCCGATGCTCGAAGCCGACCTGGGCGGAGAGACAGCCTGT 60
DB 328 GGCACCTGTCTCGACCCATGCGTCCGACCCGACCAACTGCGGCGAGAGACAGCCTGT 387
OY 61 GCCCTCCGACC 71
DB 388 GCCCTCCGACC 398
RESULT 19
AAZ60728
ID AAZ60728 standard; cDNA; 1334 BP.
XX
AC AAZ60728;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1D.
XX
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioid-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; MOR-1D; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 67..1245
FT /tag= a
FT /product= "MOR-1D"
FT /note= "no termination codon given"
XX
PN MO200004046-A2.
XX
PD 27-JAN-2000.
XX
PF 15-JUL-1999; 99WO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOAN) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
PI MPI: 2000-182402/16.
XX
DR P-PSDB; AAY68879.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 32; Fig 2B; 83pp; English.
XX
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1D. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomous nervous systems, e.g., regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to

CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1334 BP; 320 A; 397 C; 297 G; 320 T; 0 other:
Query Match 79.7%; Score 56.6; DB 21; Length 1334;
Best Local Similarity 87.3%; Pred. No. 4.2e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 GCAACCTGTCGACCCGATGCTCGAAGCCGACCTGGGCGGAGAGACAGCCTGT 60
DB 176 GCAACGAGTCCGACCCATGCGTCTTAACCGACAGGGGCTTGGCGGAGAGACAGCCTGT 235
OY 61 GCCCTCCGACC 71
DB 236 GCCCTCCGACC 246
RESULT 20
AAZ60737
ID AAZ60737 standard; cDNA; 1346 BP.
XX
AC AAZ60737;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1B I.
XX
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opioid-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; MOR-1B I; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 67..1242
FT /tag= a
FT /product= "MOR-1B I"
XX
PN MO200004046-A2.
XX
PD 27-JAN-2000.
XX
PF 15-JUL-1999; 99WO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOAN) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
PI MPI: 2000-182402/16.
XX
DR P-PSDB; AAY68886.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 46; Fig 2L-W; 83pp; English.
XX
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1B I. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that

CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1346 BP; 338 A; 398 C; 282 G; 328 T; 0 other:
Query Match 79.7%; Score 56.6; DB 21; Length 1346;
Best Local Similarity 87.3%; Pred. No. 4.2e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCGCTGGCGGAGAGACAGCCTGT 60
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCAGCGGCTTGGCGGAGACACAGCCTGT 235
QY 61 GCCCTCCGACC 71
DB 236 GCCCTCAGACC 246
RESULT 21
AA260736
ID AA260736 standard; CDNA: 1365 BP.
XX
AC AA260736;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1A.
XX
KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KW opioid-mediated ingestive response; opioid activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KW endocrine system; autonomic nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1A; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 67..1239
FT /*tag= a
FT /product= "MOR-1A"
XX
PN MO200004046-A2.
XX
PD 27-JAN-2000.
XX
PE 15-JUL-1999; 99WO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOC) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
DR WPI: 2000-182402/16.
DR P-PSDB: AAY68885.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 44; Fig 2J; 83pp; English.
XX
CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1A. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1365 BP; 341 A; 399 C; 290 G; 335 T; 0 other:
Query Match 79.7%; Score 56.6; DB 21; Length 1365;
Best Local Similarity 87.3%; Pred. No. 4.2e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCGCTGGCGGAGAGACAGCCTGT 60
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCAGCGGCTTGGCGGAGACACAGCCTGT 235
QY 61 GCCCTCCGACC 71
DB 236 GCCCTCAGACC 246
RESULT 22
AA260726
ID AA260726 standard; CDNA: 1423 BP.
XX
AC AA260726;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1C.
XX
KW Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KW opioid-mediated ingestive response; opioid activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KW endocrine system; autonomic nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1C; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 67..1383
FT /*tag= a
FT /product= "MOR-1C"
XX
PN MO200004046-A2.
XX
PD 27-JAN-2000.
XX
PE 15-JUL-1999; 99WO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOC) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
DR WPI: 2000-182402/16.
DR P-PSDB: AAY68877.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 30; Fig 2A; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1C. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 other;

SQ Query Match 79.7%; Score 56.6; DB 21; Length 1423;

Best Local Similarity 87.3%; Pred. No. 4.2e-09;

Matches 62; Conservativity 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCAACGTGTCGACCCATGCGGTCCGACCGACCGACTGGCGGGAGAGACAGCCTGT 60

DB 176 GCAACGATGTCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGGAGCCACAGCCTGT 235

OY 61 GCCCTCGACC 71

DB 236 GCCCTCAGACC 246

RESULT 23

AAZ60729

ID AAZ60729 standard; cDNA; 1542 BP.

AC AAZ60729;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1E.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KW body weight; neuroendocrine disorder; MOR-1E; ss.

XX Mus sp.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 67..1272

FT /*tag= a

FT /transl_except= (pos: 772..774, aa: Val)

FT /product= "MOR-1E"

XX MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX P-PSDB; AAY68880.

XX DR

XX PA

XX XX

PT New splice variants of the mu-opioid receptor, useful in screening for
CC selective analgesics and for regulating morphine analgesia or body
PT weight -

PS Claim 34; Fig 2C; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1E. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.

SQ Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 other;

Query Match 79.7%; Score 56.6; DB 21; Length 1542;

Best Local Similarity 87.3%; Pred. No. 4.2e-09;

Matches 62; Conservativity 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCAACGTGTCGACCCATGCGGTCCGACCGACCGACTGGCGGGAGAGACAGCCTGT 60

DB 176 GCAACGATGTCGACCCATGCGGTCTTAACCGACGGGCTTGGCGGGAGCCACAGCCTGT 235

OY 61 GCCCTCGACC 71

DB 236 GCCCTCAGACC 246

RESULT 24

AAZ60741

ID AAZ60741 standard; cDNA; 1610 BP.

AC AAZ60741;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KW body weight; neuroendocrine disorder; MOR-1; ss.

XX Mus sp.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 283..1479

FT /*tag= a

FT /transl_except= (pos: 916..918, aa: Gly)

FT /product= "MOR-1"

XX MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX P-PSDB; AAY68880.

XX DR

XX PA

XX XX

PI Pasternak G, Pan Y;
 XX
 DR WPI: 2000-182402/16.
 DR P-PSDB: AAY68889.
 XX
 PT New splice variants of the mu-opioid receptor, useful in screening for
 PT selective analgesics and for regulating morphine analgesia or body
 PT weight -
 XX
 PS Claim 29: Fig 2N, 83pp; English.
 XX
 CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
 CC splice variant MOR-1. The specification describes 11 new exons for
 CC the MOR-1 gene, which combine to yield 15 novel splice variants of
 CC the MOR-1 gene. These splice variants are potential targets for
 CC modulating morphine analgesia and opioid-mediated ingestive responses.
 CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
 CC Such compounds are potential analgesics or more generally agents that
 CC affect gastrointestinal motility, respiration or the immune, endocrine
 CC or autonomic nervous systems, e.g. regulators of peristalsis.
 CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
 CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
 CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
 CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
 CC measured to diagnose MOR-1 related pharmacological abnormalities or
 CC neuroendocrine disorders, particularly inherited disorders. Transgenic
 CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
 CC deleted, are used to study loss or gain of function phenotypes.
 CC
 XX
 S0 Sequence 1610 BP; 373 A; 476 C; 368 G; 393 T; 0 other;

Query Match 79.7%; Score 56.6; DB 21; Length 1610;
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCCGAACGCGACCGACCTGGCGGAGAGACAGCCTGT 60
 DB 392 GCAACCAATCCGACCATCGGTCTTAACCGACGGGCTTGGCGGAGACAGCCTGT 451
 QY 61 GCCCTCGACG 71
 DB 452 GCCCTCGAGAC 462

RESULT 25

AA089222
 ID AA089222 standard; cDNA; 1618 BP.

XX
 AC AA089222;

DT 20-OCT-1995 (first entry)

DE Rat mu opioid receptor cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

Location/Qualifiers
 FT Key 214..1410
 FT CDS /*tag= a

PN W09507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

XX (INDV) UNIV INDIANA FOUND.

PA
 XX Yu L;

XX
 DR WPI: 1995-131351/17.
 DR P-PSDB: AAR71964.
 XX
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 XX
 PS Disclosure; Page 190-194; 266pp; English.
 XX
 CC A 365 bp fragment of the mouse delta opioid receptor was used to
 CC screen a rat brain cDNA library under low stringency conditions.
 CC One positive clone included the sequence given in AA089222, encoding a
 CC mu opioid receptor, MOR-1 (AAR71964). MOR-1 was stably expressed in
 CC transfected CHO cells.
 XX
 S0 Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 79.7%; Score 56.6; DB 16; Length 1618;
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCATCGGTCCGAACGCGACCGACCTGGCGGAGAGACAGCCTGT 60
 DB 323 GCAACCAATCCGACCATCGGTCTTAACCGACGGGCTTGGCGGAGAGACAGCCTGT 382
 QY 61 GCCCTCGACG 71
 DB 383 GCCCTCGAGAC 393

RESULT 26

AA089223
 ID AA089223 standard; cDNA; 1618 BP.

XX
 AC AA089223;

DT 20-OCT-1995 (first entry)

DE Transcription regulatory protein cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;

transcription regulatory protein; ss.

OS Rattus sp.

Location/Qualifiers
 FT Key 339..1235
 FT CDS /*tag= a

PN W09507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

XX (INDV) UNIV INDIANA FOUND.

PA Yu L;

DR WPI: 1995-131351/17.

DR P-PSDB: AAR71965.

XX New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.

PS Disclosure; Page 199-203; 266pp; English.

XX A 365 bp fragment of the mouse delta opioid receptor was used to
 CC screen a rat brain cDNA library under low stringency conditions.

CC One positive clone included the sequence given in AA089222, encoding a
 CC mu opiod receptor, MOR-1 (AAR71964). Sequence analysis revealed an
 CC alternative reading frame (AA089223) encoding a zinc
 CC finger-containing transcription regulatory protein (AAR71965).
 XX

Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 79.7%; Score 56.6; DB 16; Length 1618;
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCACCTGTCGACCCATCGGTCCGACCGACGACCTGGGCGGAGACAGCCTGT 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 323 GCACCCAGTCGATCGGTCTGTAACCGACCGGCTGTGGCGGAGACAGCCTGT 382

QY 61 GCCCTCCGACC 71
 ||||| |||||
 Db 383 GCCCTCAGACC 393

RESULT 27

AAAS9499
 ID AAAS9499 standard; CDNA; 1618 BP.

AC AAAS9499;

DT 14-NOV-2000 (first entry)

DE CDNA encoding a mu opiod receptor polypeptide.

KW mu opiod receptor; transcription regulatory polypeptide;
 KW opiod receptor-like polypeptide; ss.

OS Rattus sp.

FT Key Location/Qualifiers
 FT CDS 214..1410
 FT /tag= a
 FT /product= "mu opiod receptor (AAB07864)"
 FT /tag= b
 FT /note= "alternative reading frame which encodes a
 FT polypeptide (AAB07865) with a zinc finger motif"

US6103492-A.

15-AUG-2000.

PF 07-JUL-1997; 97US-0889108.

PR 13-SEP-1994; 94US-0305518.

PR 08-MAR-1993; 93US-0056886.

PR 13-SEP-1993; 93US-0120601.

(INDV) UNITV INDIANA.

YU L;

WPI: 2000-542550/49.

P-PSDB: AAB07864, AAB07865.

Novel nucleic acids encoding mu opiod receptor for expressing large
 PT quantites opiod receptors which are useful for screening and
 PT evaluating subtype-selective drugs and as probes or primers -

Example 1: Column 89-92; 86pp; English.

The present sequence encodes a mu opiod receptor protein. The
 CC specification also describes a transcription regulatory polypeptide
 CC and an opiod receptor-like polypeptide. Human mu opiod receptor
 CC polynucleotides are useful as a source of probes and primers, which
 CC may be used as diagnostic tools to detect normal and abnormal DNA
 CC sequences in DNA derived from patients cells. They are also used as

CC a means for detecting and isolating other members of the polypeptide
 CC family and related polypeptides from a DNA library potentially
 CC containing such sequences. The polynucleotide is used for preparing
 CC large quantites of opiod receptor which on expression in
 CC microorganism can be useful for evaluating subtype-selective drugs.
 XX

Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 79.7%; Score 56.6; DB 21; Length 1618;
 Best Local Similarity 87.3%; Pred. No. 4.3e-09;
 Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCACCTGTCGACCCATCGGTCCGACCGACGACCTGGGCGGAGACAGCCTGT 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 323 GCACCCAGTCGATCGGTCTGTAACCGACCGGCTGTGGCGGAGACAGCCTGT 382

QY 61 GCCCTCCGACC 71
 ||||| |||||
 Db 383 GCCCTCAGACC 393

RESULT 28

AAZ60734
 ID AAZ60734 standard; CDNA; 1729 BP.

AC AAZ60734;

DT 16-MAY-2000 (first entry)

DE CDNA encoding murine mu-opiod receptor splice variant MOR-1F.

KW Mu-opiod receptor; MOR-1; splice variant; morphine analgesia;
 KW opiod-mediated ingestive response; opiod activity; analgesic;
 KW gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomous nervous system; peristalsis regulator;
 KW body weight; neuroendocrine disorder; MOR-1F; ss.

OS Mus sp.

FT Key Location/Qualifiers
 FT CDS 67..1401
 FT /tag= a
 FT /product= "MOR-1F"

WO200004046-A2.

27-JAN-2000.

PF 15-JUL-1999; 99WO-US15974.

PR 16-JUL-1998; 98US-0092980.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

Pasternak G, Pan Y;

WPI: 2000-182402/16.

P-PSDB: AAY68888.

New splice variants of the mu-opiod receptor, useful in screening for
 PT selective analgesics and for regulating morphine analgesia or body
 PT weight -

Claim 36; Fig 2F; 83pp; English.

The present sequence encodes a murine mu-opiod receptor (MOR-1)
 CC splice variant MOR-1F. The specification describes 11 new exons for
 CC the MOR-1 gene, which combine to yield 15 novel splice variants of
 CC the MOR-1 gene. These splice variants are potential targets for
 CC modulating morphine analgesia and opiod-mediated ingestive responses.
 CC The MOR-1 polypeptide is used to screen compounds for opiod activity.
 CC Such compounds are potential analgesics or more generally agents that
 CC affect gastrointestinal motility, respiration or the immune, endocrine

CC or autonomous nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1729 BP; 417 A; 505 C; 395 G; 412 T; 0 other;
Query Match 79.7%; Score 56.6; DB 21; Length 1729;
Best Local Similarity 87.3%; Pred. No. 4.3e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 60
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCGGGCTTGGCGGAGACAGCCTGT 235
OY 61 GCCCTCCGACC 71
DB 236 GCCCTCAGACC 246
RESULT 29
AAZ60735
ID AAZ60735 standard; cDNA; 2045 BP.
XX
AC AAZ60735;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1B II.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opiod-mediated ingestive response; opiod activity; analgesic;
XX gastrointestinal motility; respiration; immune system;
XX endocrine system; autonomous nervous system; peristalsis regulator;
XX body weight; neuroendocrine disorder; MOR-1B II; ss.
XX
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 67..1296
FT /*tag= a
FT /transl_except= (pos: 601..603, aa: Gly)
FT /product= "MOR-1B II"
XX
XX MO200004046-A2.
XX
XX
XX 27-JAN-2000.
XX
XX 15-JUL-1999; 99WO-US15974.
XX
XX 16-JUL-1998; 98US-0092980.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Pasternak G, Pan Y;
XX
XX WPI; 2000-182402/16.
XX
XX P-PSDB; AAY68887.
XX
XX New splice variants of the mu-opioid receptor, useful in screening for
XX selective analgesics and for regulating morphine analgesia or body
XX weight
XX
XX Claim 42; Fig 2H; 83pp; English.
XX
XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
XX splice variant MOR-1B II. The specification describes 11 new exons for
XX the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opiod-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opiod activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomous nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 2045 BP; 521 A; 526 C; 422 G; 576 T; 0 other;
Query Match 79.7%; Score 56.6; DB 21; Length 2045;
Best Local Similarity 87.3%; Pred. No. 4.4e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATGCGGTCCGAACCGCAGCCTGGCGGAGAGACAGCCTGT 60
DB 176 GCACCCAGTCCGACCCATGCGGTCTTAACCGCGGGCTTGGCGGAGACAGCCTGT 235
OY 61 GCCCTCCGACC 71
DB 236 GCCCTCAGACC 246
RESULT 30
AAF85416
ID AAF85416 standard; cDNA to mRNA; 2135 BP.
XX
XX AAF85416;
XX
XX 23-JUL-2001 (first entry)
XX
XX Nucleotide sequence of a rat mu-subtype opiate receptor.
XX
XX
XX mu-subtype opiod receptor; G protein; opiod; drug addiction; ss.
XX
XX
XX Rattus rattus.
XX
XX
XX
FH Key Location/Qualifiers
FT CDS 157..1227
FT /*tag= a
FT /product= "mu-subtype opiate receptor"
FT /transl_except= "(pos: 157..159, aa: Met)"
FT /transl_except= "(pos: 160..162, aa: Arg)"
FT /transl_except= "(pos: 163..165, aa: Ser)"
FT /transl_except= "(pos: 166..168, aa: Glu)"
FT /transl_except= "(pos: 169..171, aa: Pro)"
FT /transl_except= "(pos: 232..234, aa: Gly)"
XX
XX
XX US6225080-B1.
XX
XX
XX 01-MAY-2001.
XX
XX 28-APR-1995; 95US-0430286.
XX
XX 11-JUN-1993; 93US-0075447.
XX
XX 23-MAR-1992; 92US-0855286.
XX
XX 26-FEB-1993; 93US-0026140.
XX
XX (UHLG/) UHL G R.
XX (EPPL/) EPPLER C M.
XX (WANG/) WANG J.
XX
XX Uhl GR, Eppler CM, Wang J;
XX
XX WPI; 2001-342395/36.
XX
XX P-PSDB; AAB68440.

XX Novel isolated DNA encoding mu-subtype opioid receptor protein which is
PT useful for identifying other receptor subtypes, screening for mu opioid
PT ligands and for understanding mechanisms of opioid action
XX
PS Claim 1; Column 17-20; 51pp; English.
XX
XX The present sequence encodes a rat mu-subtype opioid receptor. The
CC polynucleotide sequence is useful for producing a mu-type opioid
CC receptor by standard recombinant techniques. The encoded protein is
CC useful for producing monoclonal or polyclonal anti-receptor antibodies
CC and to identify patterns of post-translational modifications and to
CC elucidate associated G proteins. Mu receptor polynucleotides and
CC polypeptides are useful in identifying other receptor subtypes, in
CC screening for new opioid ligands and for understanding mechanisms of
CC opioid action e.g., drug addiction.
XX
SQ Sequence 2135 BP; 541 A; 590 C; 441 G; 563 T; 0 other;
Query Match 79.7%; Score 56.6; DB 22; Length 2135;
Best Local Similarity 87.3%; Pred. No. 4.4e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACCGACTGGGGGAGAGACAGCCTGT 60
DB 140 GCAACCGAGTCCGATCGGTCTGTAACCGACCGGGCTTGGCGGAGACAGCCTGT 199
QY 61 GCCCTCCGACC 71
DB 200 GCCCTCAGACC 210
RESULT 31
AAV49252
ID AAV49252 standard; DNA; 2229 BP.
XX
AC AAV49252;
XX
DT 28-OCT-1998 (first entry)
XX
DE Mouse mu opiate receptor gene.
XX
XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 256..1452
FT /*tag= a
FT /product= "mu opiate receptor"
XX
PN MO9802534-A2.
XX
PD 22-JAN-1998.
XX
PF 11-JUL-1997; 97MO-FR01282.
XX
PR 15-JUL-1996; 96FR-0008810.
XX
PA (CNRS) CENT NAT RECH SCI.
XX
PI Dierich A, Kieffer BL, Lemeur M, Matthes HMD, Simonin FH;
XX WPI; 1998-110582/10.
DR P-PSDB; AAW4937.
XX
XX Transgenic animals defective in one type of opioid receptor - used
PT to identify agents for treatment of pain, drug addiction and
PT transplant rejection, lacking side effects of known opiate(s)
XX
PS Disclosure: Fig 11; 58pp; French.

XX This sequence represents the gene encoding the mouse mu opiate receptor
CC protein. The sequence is used to generate a transgenic non-human mammal
CC for identifying agents for treating disorders associated with opiate
CC receptors. In the mammal, the expression of the gene encoding the opiate
CC receptor is modified, particularly by the deletion of an exon and/or
CC insertion of a marker gene, e.g. the neomycin resistance gene, into the
CC sequence. Especially the expression of the gene is altered in nervous
CC tissue. The agents are potentially useful for treating severe pain
CC (chronic or acute), drug addiction and/or prevention or treatment of
CC transplant rejection (as immunosuppressants). The method may isolate and
CC identify powerful analgesics that lack morphine-like side effects.
XX
SQ Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 other;
Query Match 79.7%; Score 56.6; DB 19; Length 2229;
Best Local Similarity 87.3%; Pred. No. 4.4e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACCTGTCCGACCCATGCGGTCCGAACCGACCGACTGGGGGAGAGACAGCCTGT 60
DB 365 GCAACCGAGTCCGATCGGTCTGTAACCGACCGGGCTTGGCGGAGACAGCCTGT 424
QY 61 GCCCTCCGACC 71
DB 425 GCCCTCAGACC 435
RESULT 32
AAQ56705
ID AAQ56705 standard; cDNA; 1981 BP.
XX
AC AAQ56705;
XX
DT 15-SEP-1994 (first entry)
XX
DE Partial sequence of the murine mu-receptor clone DOR-2
DE (MOR-1, MOR-1alpha).
XX
XX Opioid receptor; morphine; opiate; ss.
XX
OS Mus musculus.
XX
PN MO9404552-A.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993; 93MO-US07665.
XX
PR 13-AUG-1992; 92US-0929200.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
XX WPI; 1994-083099/10.
XX
DR A cDNA library prep. from mouse brain was probed using DOR-1 (see
XX AAQ56704) as a probe. One clone was recovered and sequenced. This
CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised
CC to a different pattern of neurons than did DOR-1 and showed greater
CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of
CC a mu receptor was confirmed.
XX
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T; 1 other;
Query Match 75.2%; Score 53.4; DB 15; Length 1981;

XX	AAO791199;
AC	
XX	19-APR-1995 (first entry)
DT	
XX	
DE	Rat mu-subtype opioid receptor cDNA.
XX	
KM	Mu-subtype opioid receptor; MSOR; drug addiction; ds.
XX	
OS	Rattus rattus.
XX	
FH	Key Location/Qualifiers
FT	CDS 83..1154
FT	/tag= a
FT	/product= Mu-subtype_opioid_receptor
PM	
EP612845-A.	
XX	
PD	31-AUG-1994.
XX	
PF	09-FEB-1994; 94EP-0101968.
XX	
PR	26-FEB-1993; 93US-0026140.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
XX	
PI	Corbett MJ, Epler CM, Shieh H, Zysk JR;
DR	WPI: 1994-265963/33.
P-PSDB:	AAR65188.
XX	
PT	Pure mu-type opioid receptor protein - and nucleic acid coding
for it	
XX	
PS	Claim 1: Fig 11; 39pp; English.
XX	
CC	AAR65188 is the rat mu-subtype opioid receptor protein purified
from rat brain membranes, with biotinyl-D-endorphin (AAR6566)	
as its ligand. It is encoded by the nucleotide sequence AAO791199	
which was synthesised using AAO71022 and AAO71023 as PCR primers.	
AAR65188 is useful for identifying other receptor subtypes, for	
screening new opioid ligands, and for studying mechanisms of	
opioid action, e.g. drug addiction.	
CC	
Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 other;	
SQ	
Query Match	62.8%; Score 44.6; DB 15; Length 2070;
Best Local Similarity	85.9%; Pred. NO. 3e-05;
Matches 61; Conservative 0; Mismatches 9; Indels 1; Gaps	
OY	1 GCAACTGTCCGACCATTGGTTCGAGACCGACGACTGGCGGAGAGACAGCCTGT 60
Dd	76 GCATCCAGTCGCATCATCGCTGGAACCG-ACCGGGCTTGCGGGAACGACAGCCTGT 134
OY	61 GCCCTCGCAGC 71
Dd	135 GCCCTCAGACC 145
RESULT 36	
ABL33392	
ID	ABL33392 standard; DNA; 6494 BP.
XX	
AC	ABL33392;
XX	
DT	26-MAR-2002 (first entry)
XX	
XX	Human immune system associated gene SEQ ID NO: 1365.
XX	
KM	Human: Immune system disease; cytosine methylation; antisthmatic;
antiartherosclerotic; antihaemic; cytostatic; nootropic;	
neuroprotective; anti-HIV; anticoagulant; ophthalmological;	
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;	
KM	

KW	anti-inflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX	gene; ds.
OS	Homo sapiens.
PN	MO200200928-A2.
XX	
PD	03-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP07537.
XX	
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPiG-) EPIGENOMICS AG.
XX	
PI	Olek A., Piepenbrock C., Berlin K;
DR	WPI: 2002-130909/17.
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful
PT	for diagnosis and treatment of diseases associated with abnormal
PT	cytosine methylation
XX	
PS	Claim 1; SEQ ID NO 1365; 32pp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC	diseases. The present sequence is a gene of the invention.
XX	
SO	Sequence 6494 BP; 2088 A; 81 C; 1298 G; 3027 T; 0 other;
	Query Match 52.7%; Score 37.4; DB 24; Length 6494;
	Best Local Similarity 70.4%; Pred. No. 0.0068;
	Matches 50; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY	1 GCAACCTGTCCGACCCATGCGTCCGACACCGACGACTGGCGGGAGACACGCTCT 60
	1 1
DB	5320 GTAATTGTGTCATTATGCGGTTGGAATCGATTCGATTGGCGGAGAGATAGTTGT 5379
	1 1
OY	61 GCCCTCGGACC 71
	1 1 1 1 1 1 1
DB	5380 GTTTTCCGATC 5390
	1 1 1 1 1 1 1
	RESULT 37
	AA0808693/C
ID	AA0808693 standard; DNA: 109519 BP.
XX	
AC	AA0808693;
XX	
DT	26-SEP-2001 (first entry)
XX	
DE	Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.
XX	
KW	Evernimycin; antibiotic; bottle-neck gene; orthomycin;
KW	fermentation; ds.
XX	
OS	Micromonospora carbonacea var. africana.
XX	
FH	Key Location/Qualifiers
FT	CDS complement (132..1382)
FT	/*tag= a
FT	/product= "Evda"
FT	complement (1389..1394)
FT	/*tag= b

FT	CDS	complement (1490..2611)	FT	RBS	/product= "EvrC"
FT		/*tag= c	FT		22736..22740
FT	RBS	/product= "EvdB"	FT	CDS	/*tag= ad
FT		complement (2618..2622)	FT		complement (24177..25223)
FT	CDS	/*tag= d	FT		/*tag= ae
FT		complement (2622..3860)	FT	RBS	/product= "EvrH"
FT		/*tag= e	FT		complement (25230..25233)
FT	RBS	/product= "EvdC"	FT		/*tag= af
FT		complement (3867..3870)	FT	CDS	25550..26626
FT		/*tag= f	FT		/*tag= ag
FT	CDS	4143..5312	FT		/product= "EvrI"
FT		/*tag= g	FT	CDS	26685..30479
FT	RBS	/product= "EvdD"	FT		/*tag= ah
FT		4134..4138	FT		/product= "EvrJ"
FT		/*tag= h	FT	RBS	26672..26676
FT	CDS	5309..6235	FT		/*tag= ai
FT		/*tag= i	FT	CDS	complement (30557..31876)
FT		/product= "EvdE"	FT		/*tag= aj
FT		6232..7275	FT	RBS	/product= "EvrK"
FT		/*tag= j	FT		complement (31885..31888)
FT	RBS	/product= "EvdF"	FT		/*tag= ak
FT		6226..6229	FT	CDS	complement (31941..32882)
FT		/*tag= k	FT		/*tag= al
FT	CDS	7272..8327	FT		/product= "EvrL"
FT		/*tag= l	FT		complement (33167..34405)
FT		/product= "EvdG"	FT	CDS	/*tag= am
FT		8342..9364	FT		/product= "EvrM"
FT	CDS	/*tag= m	FT	RBS	complement (34414..34418)
FT		/product= "EvdH"	FT		/*tag= an
FT		8333..8336	FT	CDS	complement (34449..35210)
FT	RBS	/*tag= n	FT		/*tag= ao
FT		complement (9463..10224)	FT		/product= "EvrN"
FT	CDS	/*tag= o	FT	RBS	complement (35219..35221)
FT		/product= "EvdI"	FT		/*tag= ap
FT		complement (10232..10235)	FT	CDS	complement (35294..36238)
FT		/*tag= p	FT		/*tag= aq
FT	CDS	10424..11176	FT		/product= "EvrO"
FT		/*tag= q	FT	CDS	complement (36235..36963)
FT		/product= "EvdJ"	FT		/*tag= ar
FT		12027..12455	FT		/product= "EvrP"
FT	CDS	/*tag= r	FT	CDS	complement (36998..38026)
FT		/product= "EvdK"	FT		/*tag= as
FT		/partial	FT		/product= "EvrQ"
FT		/note= "No start codon"	FT	CDS	complement (38072..38566)
FT	CDS	complement (12108..13022)	FT		/*tag= at
FT		/*tag= s	FT		/product= "EvrR"
FT	RBS	/product= "EvdL"	FT	CDS	complement (38892..40163)
FT		complement (13027..13030)	FT		/*tag= au
FT		/*tag= t	FT	CDS	/product= "EvrS"
FT	CDS	complement (14410..15363)	FT		complement (40216..40890)
FT		/*tag= u	FT		/*tag= av
FT		/product= "EvrA"	FT		/product= "EvrT"
FT	RBS	complement (15369..15373)	FT		complement (40899..40902)
FT		/*tag= v	FT	RBS	/*tag= aw
FT	CDS	complement (15380..16414)	FT		complement (40887..41576)
FT		/*tag= w	FT		/*tag= ax
FT		/product= "EvrB"	FT	CDS	/product= "EvrU"
FT		complement 16419..17873	FT		complement (41679..42707)
FT	CDS	/*tag= x	FT		/*tag= ay
FT		/product= "EvrC"	FT		/product= "EvrV"
FT	CDS	complement (17870..18934)	FT	RBS	complement (42714..42717)
FT		/*tag= y	FT		/*tag= az
FT		/product= "EvrD"	FT	CDS	complement (42810..43799)
FT	CDS	19374..20906	FT		/*tag= ba
FT		/*tag= z	FT		/product= "EvrW"
FT		/product= "EvrE"	FT	RBS	complement (43807..43811)
FT	CDS	21064..22542	FT		/*tag= bb
FT		/*tag= aa	FT	CDS	complement (43799..44866)
FT	RBS	/product= "EvrF"	FT		/*tag= bc
FT		21056..22542	FT		/product= "EvrX"
FT		/*tag= ab	FT	CDS	complement (45014..45760)
FT	CDS	22748..24172	FT		/*tag= bd
FT		/*tag= ac	FT		/product= "EvrY"

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FT RBS complement (45767..45770)
FT CDS /*tag= be
FT CDS complement (45962..46714)
FT /*tag= bf
FT product= "Evr2"
FT RBS complement (45952..45956)
FT /*tag= bg
FT CDS complement (47156..49234)
FT /*tag= bh
FT product= "EvsA"
FT CDS 51627..52715
FT /*tag= bi
FT product= "EvsB"
FT RBS 51629..51622
FT /*tag= bj
FT CDS 52889..53557
FT /*tag= bk
FT product= "EvsC"
FT CDS 53554..54207
FT /*tag= bl
FT product= "EvsA"
FT CDS complement (54362..55117)
FT /*tag= bm
FT product= "EvsB"
FT RBS complement (55125..55128)
FT /*tag= bn
FT CDS complement (55135..56094)
FT /*tag= bo
FT product= "EvsC"
FT RBS complement (56100..56103)
FT /*tag= bp
FT CDS complement (56184..56813)
FT /*tag= bq
FT product= "EvsC2"
FT 56961..58709
FT CDS
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Query Match 37.28; Score 26.4; DB 22; Length 109519;
Best Local Similarity 65.0%; Pred. No. 30;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 11 CGACCCATGCGGTCCGAACCGCAGCAGCTGGGGGAGAGACACGCTGTCCTCCGAC 70
Db 9489 CGACCTGTGGCTGCAGACGGAGCTGACCTGGCGGGCGCGGTGTGGACCGCGAC 9430

RESULT 38
AAK93041
ID AAK93041 standard; cDNA: 527 BP.

AC AAK93041;

DT 06-NOV-2001 (first entry)

DE Human cDNA 3'-end sequence, SEQ ID NO: 1501.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

PA (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

```
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX Claim 3; SEQ ID NO 1501; 1380bp + sequence listing; English.
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is the nucleotide
XX sequence of the 3'-end of a cDNA provided in the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
```

Query Match 36.18; Score 25.6; DB 22; Length 527;
Best Local Similarity 66.1%; Pred. No. 31;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 GCACCTGTCCGATGCGGTCCGAACCGCAGCAGCTGGGGGAGAGACAGC 56
Db 39 GCACACTGCCCTTCCAGGTGGGTGAACCCACGACGAGGAGGAGAGATGC 94

RESULT 39
AAC90469/c
ID AAC90469 standard; cDNA: 1178 BP.

AC AAC90469;

DT 12-MAR-2001 (first entry)

DE Human uncoupling protein cDNA #18.

KW Human; uncoupling protein; immunosuppressive; antiarthritic;

KW antirheumatic; antiproliferative; cardiant; vasotropic;

KW cerebroprotective; neuroprotective; antibacterial; optalmological;

KW gastrointestinal; nephroprotective; gynaecological; vulnerrary; thrombolytic;

KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;

KW infertility; ss.

OS Homo sapiens.

PN WO200061614-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09534.

PR 09-APR-1999; 99US-0128701.

PR 08-JUL-1999; 99US-0142821.

PR 18-AUG-1999; 99US-0149448.

PR 12-NOV-1999; 99US-0164751.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR;
WPI; 2000-656322/63.
P-PSDB; AAB50395.

Uncoupling proteins and nucleic acid sequences encoding them, useful
for detecting, preventing and treating proliferative, neurological,
immune system, cardiovascular and gastrointestinal disorders -

PS Claim 1; Page 315-316; 343pp; English.
XX
CC The present sequence is one of eighteen isolated nucleotide sequences
CC encoding uncoupling proteins. The nucleotide sequences may be used for
CC the detection of various disorders such as cancer, for chromosome
CC identification, as chromosome markers and for numerous other diagnostic
CC or research purposes. The uncoupling protein encoded by the nucleotide
CC sequences may be used to treat disorders such as neural, immune,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders, wounds, infectious diseases,
CC thrombosis, arthritis, and infertility.
XX
SQ Sequence 1178 BP; 239 A; 388 C; 329 G; 222 T; 0 other:
XX
Query Match 36.1%; Score 25.6; DB 21; Length 1178;
Best Local Similarity 66.1%; Pred. No. 34;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGACAGC 56
DB 1074 GCACACTGCGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGATGTC 1019
RESULT 40
AA160768
ID AA160768 standard; cDNA; 1856 BP.
XX
AC AA160768;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 4757.
XX
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PE 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HSE-) HXSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Mehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR P-PSDB: AAM41612.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
XX as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 4757; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic;

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 1856 BP; 370 A; 572 C; 611 G; 303 T; 0 other:
XX
Query Match 36.1%; Score 25.6; DB 22; Length 1856;
Best Local Similarity 66.1%; Pred. No. 35;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 1 GCACCTGTCCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGACAGC 56
DB 51 GCACACTGCGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGGATGTC 106
RESULT 41
AAK94578/C
ID AAK94578 standard; cDNA; 1872 BP.
XX
AC AAK94578;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human full-length cDNA, SEQ ID NO: 3500.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PE 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI: 2001-524255/58.
DR P-PSDB: AAM93644.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 3500; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 1872 BP; 294 A; 621 C; 588 G; 369 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 1872;

Best Local Similarity 66.1%; Pred. No. 35;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

YY 1 GCAACCTGTCGACCGATGCGGTCCGACCGACCGACTGGCGGAGAGACAGC 56

DB 1834 GCACACTGCGCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGAGATGC 1779

RESULT 42

AA158982/c

AA158982 standard; cDNA; 2003 BP.

AA158982;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 1185.

Human: neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokine; thrombolytic; drug screening; arthritis; inflammation;
leukemia; ss.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000MO-US34263.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao QA, Zhou P, Goodrich R, Drmanac RR;

WPI; 2001-442253/47.

P-PSDB; AAM39826.

Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -

Claim 1; SEQ ID NO 1185; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and
the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
centralised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: immune system suppression,
activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 2003 BP; 311 A; 659 C; 650 G; 383 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 2003;

Best Local Similarity 66.1%; Pred. No. 36;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

YY 1 GCAACCTGTCGACCGATGCGGTCCGACCGACCGACTGGCGGAGAGACAGC 56

DB 1953 GCACACTGCGCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGAGATGC 1898

RESULT 43

AAF27736/c

AAF27736 standard; cDNA; 2004 BP.

AAF27736;

28-MAR-2001 (first entry)

Human transport protein TPPT-36 coding sequence.

Human: transport protein; TPPT; transport disorder; metabolic disorder;
neurological disorder; cardiovascular disorder; reproductive disorder;
immune disorder; cancer; ss.

Homo sapiens.

WO200078953-A2.

28-DEC-2000.

16-JUN-2000; 2000MO-US16668.

17-JUN-1999; 99US-0139923.

10-AUG-1999; 99US-0148177.

18-AUG-1999; 99US-0149357.

28-OCT-1999; 99US-0162287.

(INCY-) INCYTE GENOMICS INC.

Lai P, Yang J, Yue H, Hillman JL, Tang YT, Bandman O, Burford N;
Baughn MR, Azimzai Y, Lu DM, Au-Young J, Patterson C;

WPI; 2001-041424/05.

P-PSDB; AAB60116.

Isolated polypeptide with a human transport protein sequence is useful
for the diagnosis, prevention and treatment of disorders associated
with the immune, reproductive and cardiovascular systems -

Claim 5; Page 161-162; 165pp; English.

The present invention provides the protein and coding sequences for 43
novel human transport proteins (designated TPPTs). These can be used in
the diagnosis and treatment of transport, metabolic, neurological,
reproductive, cardiovascular and immune disorders, and cell proliferative
disorders such as cancer.

Sequence 2004 BP; 314 A; 659 C; 650 G; 381 T; 0 other;

Query Match 36.1%; Score 25.6; DB 22; Length 2004;

Best Local Similarity 66.1%; Pred. No. 36;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

YY 1 GCAACCTGTCGACCGATGCGGTCCGACCGACCGACTGGCGGAGAGACAGC 56

DB 1951 GCACACTGCGCTTCCAGGTGGGTGAAGCCAGCAGCAGGAGGAGAGATGC 1896

XX XX Human cardiovascular system antigen genomic DNA SEQ ID No 1384.
DE XX
XX XX Cardiovascular system antigen: human; mouse; rabbit; goat; horse; cat;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW antihemematic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; vitucide; fungicide; cancer;
KW ophthalmological; vulnerrary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; tissue regeneration;
KW anti-fertility.
XX XX
OS Homo sapiens.
XX XX
PN WO200155321-A2.
PD
XX 02-AUG-2001.
PF
XX 17-JAN-2001; 2001WO-US01340.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241821.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.

KW dermatological; neuroprotective;thrombolytic; coagulant; neotropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.
 XX
 OS Homo sapiens.
 PN WO200055350-A1.
 XX
 PD 21-SEP-2000.
 XX
 XX 08-MAR-2000; 2000WO-00505882.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-567533/55.
 DR P-PSDB: AAB43515.
 XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 XX useful for treating or diagnosing e.g. cancer -
 XX
 SS Claim 1; Page 703-704; 2352pp; English.

CC	AA07760 to AAC78448 encode the human cancer associated proteins given
CC	in A0443398 to A0444239. The proteins can have activities based on the
CC	tissues and cells the genes are expressed in. Example of activities
CC	include: cytostatic; proliferative; vulnerary; immunomodulator;
CC	antidiabetic; antisthmatic; antineumatic; antibacterial;
CC	antihistaminatory; antihyroid; antiallergic; antitubercular; antiviral;
CC	dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC	neotropic; vasotropic; antipsoriatic and antiangiogenic. The
CC	polynucleotides and polypeptides can be used for preventing, treating or
CC	ameliorating medical conditions and diagnosing pathological conditions.
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC	the present invention may be used to treat immune disorders by activating
CC	or inhibiting the proliferation, differentiation or mobilisation of
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune
CC	disorders, allergic reactions, graft versus host disease and organ
CC	rejection, modulate haemostatic or thrombolytic activity, modulate
CC	inflammation, cancers, cardiovascular disorders, neurological disease and
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to
CC	AAC78457 and A0444240 represent sequences used in the exemplification of
CC	the present invention.
XX	
XX	
SO	Sequence 2053 BP; 393 A; 608 C; 610 G; 436 T; 6 other;
Query Match	34.9%; Score 24.8; DB 21; Length 2053;
Best Local Similarity	60.3%; Pred. No. 64;
Matches	41; Conservative 0; Mismatches 27; Indels 0; Gaps 0
OY	4 ACGTGTCCGACCATGGCGTCCGACCGCAGCTGTGGCGGAGACAGACCTGTGCC 63
Db	963 ACGTGTAGCCCTTCTCCCTCCGCGCAGCTCTCAGCGACCGAGGCCCTCTCTGTGGC 904
OY	64 CTCGACC 71
Db	903 CTCGAGC 896
RESULT 49	
AAZ24407/c	
ID	AAZ24407 standard; cDNA; 2190 BP.
XX	
XX	AAZ24407;
DT	14-FEB-2000 (first entry)

DE	Human bladder tumour cDNA library derived EST 19.
XX	
XX	Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
KW	treatment; gene therapy; EST; ss.
XX	
OS	Homo sapiens.
XX	
EN	DE19818619-A1.
XX	
PD	28-OCT-1999.
XX	
PF	21-APR-1998; 98DE-1018619.
XX	
ER	21-APR-1998; 98DE-1018619.
XX	
PA	(META-) METAGEN GES. GENOMFORSCHUNG MBH.
XX	
PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX	
DR	WPI; 1999-612028/53.
XX	
PT	New nucleic acid sequences expressed in bladder tumor tissue, and
XX	derived polypeptides, for treatment of bladder tumor and identification
PT	of therapeutic agents -
XX	
SS	Claim 3; Page 74-75; 132pp; German.

This invention describes novel polypeptide fragments (I) and the CC polynucleotides (II) that encode them that are highly expressed in a CC human bladder tumour and which have cytostatic activity. (II) are used CC for recombinant expression of (I) and to isolate complete genes. (I) are CC used to identify agents suitable for treatment of bladder cancer, to CC directly treat this form of cancer (including expression from gene CC therapy vectors) or are used in a preparation for cancer treatment. (I) CC is also used for the generation of specific antibodies. (II) are CC identified by assembling ESTs (expressed sequence tags) from a CC particular tissue type before comparison of expression patterns. This CC allows a significantly longer fragment of the gene to be revealed, and CC therefore reduces the number of failures associated with the fact that CC ESTs from different libraries may represent different parts of the same CC unknown gene, distorting the estimated frequency of occurrence in a CC particular tissue. AA23260-243309 represent expressed sequence tag (EST) CC fragments isolated from a human bladder tumour cDNA library which encode CC the proteins represented in AY66143-Y66198.

XX Sequence 2190 BP; 430 A; 623 C; 653 G; 484 T; 0 other:

XX

Query Match 34.9%; Score 24.8; DB 20; Length 2190;

Best Local Similarity 60.3%; Pred. No. 65;

Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 4 ACCTGTCGACCATTGCGGTCCGAACCGCACCGACCTGGCGGAGACAGACCTGTGCC 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1123 ACCTGCTACGCCCTTCCTCCCTCCGGCCAGCGCTTAGCCACACGAGGCCCTCTGTGGC 1064
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 64 CTCGAGC 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1063 CTCGAGC 1056

RESULT 50
AA248077/C
ID AA248077 standard; DNA: 4351 BP.
XX
XX AA248077;
AC
XX
DT 08-MAR-2000 (first entry)
XX
DE Human insulin like growth factor II exons 7 to 9 nucleotide sequence.
XX
XX Human IGF-II; insulin-like growth factor II; cell growth modulation;
XX tumour inhibition; antisense oligonucleotide; phosphorothiolate;
TW

KW metastasis; antitumour; antiproliferative; angiogenesis; apoptosis;
KW tumour cell migration; proliferative disease; atherosclerosis;
KW psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO955854-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-CA00323.
XX
PR 23-APR-1998; 98US-0082791.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 2000-062027/05.
XX
PT Antisense oligonucleotides against mRNA of insulin-like growth factor
PI II, for treating tumors and other proliferative diseases
XX
PS Disclosure; Fig 11D; 72pp; English.
XX
CC AA248041 to AA248070 represent specifically claimed antisense
CC oligonucleotides (i) complementary to the mRNA of human insulin-like
CC growth factor II (IGF-II). The present invention also describes a method
CC for inhibiting growth or metastasis of mammalian tumours by
CC administering (i). (i) have antitumour and antiproliferative activity,
CC and inhibits: (i) the autocrine and paracrine functions of IGF-II which
CC promote tumour-induced angiogenesis and tumour cell migration; and (ii)
CC autocrine growth of tumour cells, possibly including induction of
CC apoptosis. (i) may also function as ribozymes. (i) are used for
CC inhibiting growth and metastasis of mammalian tumours, also: (i) for
CC treatment of other proliferative diseases, e.g. atherosclerosis and
CC psoriasis; (ii) when labeled, as probes for detecting IGF-II mRNA; and
CC (iii) as molecular weight markers. (i) that bind to the 5'-untranslated
CC region of the foetal transcript (the form present in tumour cells) should
CC not affect the adult transcript. They are effective against
CC drug-resistant tumours. The present sequence represents exons 7 to 9 of
CC the human IGF-II, from the present invention.
XX
SQ Sequence 4351 BP: 1073 A; 1431 C; 1053 G; 794 T; 0 other;

Query Match 34.9%; Score 24.8; DB 21; Length 4351;
Best Local Similarity 60.3%; Pred. No. 69;
Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 4 ACCGTCCGACCCATGCGTCCGAACCGACGACTGGCGGAGAGACAGACCTGTGCG 63
DB 3386 ACCTCTGTAGCCCTTCCTCCGCGACGCTAGGCCACGAGCCGCCCTCTGTGTGCG 3327
OY 64 CTCGAGCC 71
DB 3326 CTCGAGCC 3319

Search completed: November 1, 2002, 15:32:02
Job time : 320 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:18:01 : Search time 45 Seconds
(without alignments)
387.555 Million cell updates/sec

Title: US-09-626-616-7_COPY_354_424
Perfect score: 71
Sequence: 1 GCACCTGTGCGACCATGC.....ACAGCTGTGCGCTCGACG 71

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 328456

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents-NA: *
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	ID	Description
1	71	100.0	1610	3	US-08-889-108-7
2	71	100.0	1610	5	PCT-US94-10358-7
3	69.4	97.7	2160	4	US-08-188-275A-1
4	69.4	97.7	2162	4	US-09-351-198-1
5	69.4	97.7	2162	4	US-09-113-426-1
6	56.6	79.7	1618	3	US-08-889-108-1
7	56.6	79.7	1618	3	US-08-889-108-1
8	56.6	79.7	1618	4	US-08-889-108-3
9	56.6	79.7	1618	4	US-08-120-601B-1
10	56.6	79.7	1618	5	US-08-120-601B-3
11	56.6	79.7	1618	5	PCT-US94-10358-1
12	56.6	79.7	2135	5	PCT-US94-10358-3
13	53.4	75.2	1981	4	US-08-430-286A-1
14	24.2	34.1	1728	4	US-08-387-707-15
15	24.2	34.1	41804	4	US-09-171-461-29
16	24.2	34.1	367	2	US-08-727-688-1
17	24	33.8	1297	2	US-08-727-688-9
18	24	33.8	1524	4	US-09-020-956-109
19	24	33.8	1524	4	US-09-030-607-109
20	24	33.8	1524	4	US-09-439-313-109
21	23.8	33.5	2181	3	US-09-129-075-3
22	23.8	33.5	2181	4	US-09-346-237-12
23	23.6	33.2	2156	1	US-08-012-988A-1
24	23.2	32.7	6855	4	US-09-404-650-1
25	23.2	32.7	6855	4	US-09-404-650-3
26	23	32.4	502	4	US-09-030-607-195
27	23	32.4	502	4	US-09-439-313-195

28	23	32.4	1375	2	US-08-468-812-1	Sequence 1, Appli
29	23	32.4	1375	5	US-08-590-563-1	Sequence 1, Appli
30	22.8	32.1	1335	5	PCT-US91-06532-1	Sequence 1, Appli
31	22.8	32.1	50341	1	US-08-247-901C-1	Sequence 1, Appli
32	22.8	32.1	50341	2	US-09-075-906-1	Sequence 1, Appli
33	22.8	32.1	52297	4	US-09-426-436-1	Sequence 1, Appli
34	22.8	32.1	52297	4	US-08-705-557-1	Sequence 1, Appli
35	22.8	32.1	4403765	4	US-09-103-840A-2	Sequence 2, Appli
36	22.8	32.1	4411529	4	US-09-103-840A-1	Sequence 1, Appli
37	22.6	31.8	4732	5	PCT-US93-06251-22	Sequence 22, Appli
38	22.6	31.8	4736	4	US-09-056-105-12	Sequence 12, Appli
39	22.6	31.8	4741	4	US-09-056-105-11	Sequence 11, Appli
40	22.6	31.8	13842	4	US-09-105-537-30	Sequence 30, Appli
41	22.6	31.8	30001	1	US-08-125-468-1	Sequence 1, Appli
42	22.6	31.8	30001	2	US-08-474-933-1	Sequence 1, Appli
43	22.6	31.8	36519	3	US-08-922-137-2	Sequence 2, Appli
44	22.6	31.8	36778	4	US-09-105-537-5	Sequence 5, Appli
45	22.6	31.8	38506	4	US-09-320-878-19	Sequence 19, Appli
46	22.6	31.8	50937	4	US-09-428-517-1	Sequence 1, Appli
47	22.4	31.5	1452	3	US-09-170-331-3	Sequence 3, Appli
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49	22.2	31.3	382	2	US-08-592-541-96	Sequence 96, Appli
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51	22.2	31.3	382	4	US-09-127-480-96	Sequence 96, Appli
52	22.2	31.3	382	4	US-08-496-841C-96	Sequence 96, Appli
53	22.2	31.3	3150	4	US-09-522-666-5	Sequence 5, Appli
54	22.2	31.3	3150	1	US-08-131-365B-53	Sequence 53, Appli
55	22.2	31.3	5197	2	US-08-668-123-53	Sequence 53, Appli
56	22.2	31.3	4411529	4	US-09-103-840A-1	Sequence 1, Appli
57	22	31.0	653	4	US-09-439-313-363	Sequence 363, App
58	22	31.0	50937	4	US-09-428-517-1	Sequence 1, Appli
59	21.8	30.7	643	4	US-08-861-774E-53	Sequence 53, Appli
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62	21.8	30.7	1024	4	US-09-143-068-3	Sequence 3, Appli
63	21.8	30.7	1024	4	US-09-202-089-3	Sequence 3, Appli
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65	21.8	30.7	1211	2	US-08-997-362-40	Sequence 40, Appli
66	21.8	30.7	1211	3	US-08-872-970-40	Sequence 40, Appli
67	21.8	30.7	1211	4	US-09-095-855-40	Sequence 40, Appli
68	21.8	30.7	1211	4	US-08-705-347A-40	Sequence 40, Appli
69	21.8	30.7	1211	4	US-09-324-542-40	Sequence 40, Appli
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73	21.6	30.4	3107	2	US-08-813-940-3	Sequence 3, Appli
74	21.6	30.4	3381	4	US-09-009-119-1	Sequence 1, Appli
75	21.6	30.4	3381	4	US-09-371-507-1	Sequence 1, Appli
76	21.6	30.4	3546	1	US-07-951-715A-10	Sequence 10, Appli
77	21.6	30.4	3546	1	US-07-951-715A-12	Sequence 12, Appli
78	21.6	30.4	3546	1	US-07-951-715A-14	Sequence 14, Appli
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80	21.6	30.4	3546	2	US-08-455-448A-12	Sequence 12, Appli
81	21.6	30.4	3546	2	US-08-455-448A-14	Sequence 14, Appli
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89	21.6	30.4	3546	3	US-08-455-444-12	Sequence 12, Appli
90	21.6	30.4	3546	3	US-08-455-444-14	Sequence 14, Appli
91	21.6	30.4	3546	4	US-09-547-422-10	Sequence 10, Appli
92	21.6	30.4	3546	4	US-09-547-422-12	Sequence 12, Appli
93	21.6	30.4	3546	4	US-09-547-422-14	Sequence 14, Appli
94	21.6	30.4	4897	6	US-08-814-095-7	Sequence 7, Appli
95	21.6	30.4	35060	6	US-09-103-840A-2	Sequence 2, Appli
96	21.6	30.4	4403765	4	US-08-817-997A-1	Sequence 1, Appli
97	21.4	30.1	994	1	US-08-933-750C-77	Sequence 77, Appli
98	21.4	30.1	1107	3	US-09-234-613-77	Sequence 77, Appli
99	21.4	30.1	1107	3	US-09-067-351-5	Sequence 5, Appli
100	21.4	30.1	2167	2		

101	21.4	30.1	2167	4	US-09-360-490-5	Sequence 5, Appl1	c 174	20.6	29.0	6854	4	US-09-194-905-7	Sequence 7, Appl1
c 102	21.4	30.1	2403	2	US-08-700-813B-26	Sequence 26, Appl1	175	20.6	29.0	17612	3	US-08-911-853-29	Sequence 29, Appl1
c 103	21.4	30.1	2817	2	US-08-655-836-4	Sequence 4, Appl1	176	20.6	29.0	17612	4	US-09-479-409-29	Sequence 29, Appl1
c 104	21.4	30.1	2817	2	US-09-020-753-4	Sequence 4, Appl1	177	20.6	29.0	17612	4	US-09-479-453-29	Sequence 29, Appl1
c 105	21.4	30.1	7888	4	US-08-984-709A-49	Sequence 49, Appl1	c 178	20.4	28.7	495	4	US-09-020-956-94	Sequence 94, Appl1
c 106	21.2	29.9	190	4	US-09-437-457-5	Sequence 5, Appl1	c 179	20.4	28.7	495	4	US-09-030-607-94	Sequence 94, Appl1
c 107	21.2	29.9	342	4	US-08-905-223-196	Sequence 196, App	c 180	20.4	28.7	495	4	US-09-439-313-94	Sequence 94, Appl1
c 108	21.2	29.9	702	1	US-08-458-568A-3	Sequence 3, Appl1	c 181	20.4	28.7	503	4	US-08-483-533-7	Sequence 7, Appl1
c 109	21.2	29.9	2639	6	US-07-952-817-8	Sequence 8, Appl1	c 182	20.4	28.7	503	4	US-09-283-471A-7	Sequence 7, Appl1
c 110	21.2	29.9	2639	6	5210025-1	Patent No. 5210025	c 183	20.4	28.7	617	4	US-09-328-111-846	Sequence 846, App
c 111	21.2	29.9	11604	4	US-09-385-028-13	Sequence 13, Appl1	c 184	20.4	28.7	751	1	US-08-474-177-15	Sequence 15, Appl1
c 112	21.2	29.9	12001	1	US-08-458-568A-11	Sequence 11, Appl1	c 185	20.4	28.7	751	1	US-08-487-033-15	Sequence 15, Appl1
c 113	21.2	29.9	15079	4	US-09-385-028-1	Sequence 1, Appl1	c 186	20.4	28.7	751	1	US-08-480-810-15	Sequence 15, Appl1
c 114	21	29.6	351	4	US-09-085-1998-41	Sequence 41, Appl1	c 187	20.4	28.7	751	2	US-08-508-735-15	Sequence 15, Appl1
c 115	21	29.6	641	6	546585-6	Patent No. 546585	c 188	20.4	28.7	751	2	US-08-448-251-15	Sequence 15, Appl1
c 116	21	29.6	777	4	US-08-998-416-212	Sequence 212, App	c 189	20.4	28.7	751	2	US-08-486-047-15	Sequence 15, Appl1
c 117	21	29.6	783	1	US-08-264-861A-11	Sequence 11, Appl1	c 190	20.4	28.7	751	3	US-09-120-130-15	Sequence 15, Appl1
c 118	21	29.6	783	5	PCT-US95-07784-11	Sequence 11, Appl1	c 191	20.4	28.7	751	3	US-09-115-252-15	Sequence 15, Appl1
c 119	21	29.6	1150	1	US-08-264-861A-11	Sequence 10, Appl1	c 192	20.4	28.7	751	3	US-08-986-515-15	Sequence 15, Appl1
c 120	21	29.6	1150	1	PCT-US95-07784-10	Sequence 10, Appl1	c 193	20.4	28.7	751	3	US-09-120-128-15	Sequence 15, Appl1
c 121	21	29.6	1678	6	5223391-1	Patent No. 5223391	c 194	20.4	28.7	751	4	US-09-120-129-15	Sequence 15, Appl1
c 122	21	29.6	2364	2	US-08-981-690-1	Sequence 1, Appl1	c 195	20.4	28.7	751	4	US-09-201-139-15	Sequence 15, Appl1
c 123	21	29.6	2547	3	US-08-508-761B-1	Sequence 1, Appl1	c 196	20.4	28.7	751	4	US-09-120-131-15	Sequence 15, Appl1
c 124	21	29.6	3247	4	US-09-487-368A-3	Sequence 3, Appl1	c 197	20.4	28.7	751	4	US-08-998-416-467	Sequence 467, App
c 125	21	29.6	4622	4	US-08-509-024-6	Sequence 6, Appl1	c 198	20.4	28.7	796	4	US-08-836-075A-65	Sequence 65, Appl1
c 126	21	29.6	4622	4	US-09-333-279-6	Sequence 6, Appl1	c 199	20.4	28.7	831	2	US-08-865-337A-4	Sequence 4, Appl1
c 127	21	29.6	7286	5	PCT-US95-11684-1	Sequence 1, Appl1	c 200	20.4	28.7	1108	2	PCT-US93-03035-1	Sequence 1, Appl1
c 128	20.8	29.3	553	2	US-08-474-020A-14	Sequence 14, Appl1	c 201	20.4	28.7	1165	3	US-09-036-987A-32	Sequence 32, Appl1
c 129	20.8	29.3	573	5	US-08-290-665A-112	Sequence 112, App	c 202	20.4	28.7	1165	4	US-09-370-700-32	Sequence 32, Appl1
c 130	20.8	29.3	573	5	PCT-US95-10398-112	Sequence 112, App	c 203	20.4	28.7	1280	4	US-08-483-533-38	Sequence 38, Appl1
c 131	20.8	29.3	650	1	US-08-229-515A-13	Sequence 13, Appl1	c 204	20.4	28.7	1280	4	US-09-283-471A-38	Sequence 38, Appl1
c 132	20.8	29.3	650	1	US-08-645-865-13	Sequence 13, Appl1	c 205	20.4	28.7	1280	4	US-08-483-533-37	Sequence 37, Appl1
c 133	20.8	29.3	1368	2	US-08-738-172-3	Sequence 3, Appl1	c 206	20.4	28.7	1292	4	US-08-483-533-37	Sequence 37, Appl1
c 134	20.8	29.3	1521	1	US-08-083-948-14	Sequence 14, Appl1	c 207	20.4	28.7	1300	4	US-08-483-533-39	Sequence 39, Appl1
c 135	20.8	29.3	1521	1	US-08-393-785-14	Sequence 14, Appl1	c 208	20.4	28.7	1300	4	US-09-283-471A-39	Sequence 39, Appl1
c 136	20.8	29.3	1521	1	US-08-475-694-14	Sequence 14, Appl1	c 209	20.4	28.7	1307	4	US-08-483-533-36	Sequence 36, Appl1
c 137	20.8	29.3	1521	1	US-08-712-057-14	Sequence 14, Appl1	c 210	20.4	28.7	1327	4	US-09-283-471A-36	Sequence 36, Appl1
c 138	20.8	29.3	1524	2	US-08-716-942-24	Sequence 24, Appl1	c 211	20.4	28.7	1472	1	US-08-333-565-1	Sequence 1, Appl1
c 139	20.8	29.3	1647	1	US-08-083-948-13	Sequence 13, Appl1	c 212	20.4	28.7	1472	2	US-08-661-479-1	Sequence 1, Appl1
c 140	20.8	29.3	1647	1	US-08-393-785-13	Sequence 13, Appl1	c 213	20.4	28.7	1483	4	US-09-262-749-1	Sequence 1, Appl1
c 141	20.8	29.3	1647	1	US-08-475-694-13	Sequence 13, Appl1	c 214	20.4	28.7	1553	3	US-09-022-669-1	Sequence 1, Appl1
c 142	20.8	29.3	1647	1	US-08-712-057-13	Sequence 13, Appl1	c 215	20.4	28.7	1620	3	US-08-985-950-11	Sequence 11, Appl1
c 143	20.8	29.3	1865	1	US-08-083-948-7	Sequence 7, Appl1	c 216	20.4	28.7	1777	1	US-08-173-508-5	Sequence 5, Appl1
c 144	20.8	29.3	1865	1	US-08-393-785-7	Sequence 7, Appl1	c 217	20.4	28.7	1777	2	US-08-665-310-5	Sequence 5, Appl1
c 145	20.8	29.3	1865	1	US-08-475-694-7	Sequence 7, Appl1	c 218	20.4	28.7	1777	2	US-08-951-182-2	Sequence 2, Appl1
c 146	20.8	29.3	1865	1	US-08-712-057-7	Sequence 7, Appl1	c 219	20.4	28.7	1926	2	US-08-978-182-2	Sequence 2, Appl1
c 147	20.8	29.3	2150	3	US-09-263-023-1	Sequence 1, Appl1	c 220	20.4	28.7	1926	2	US-09-205-681-2	Sequence 2, Appl1
c 148	20.8	29.3	2150	3	US-09-381-849-2	Sequence 2, Appl1	c 221	20.4	28.7	2196	2	US-08-865-337A-2	Sequence 2, Appl1
c 149	20.8	29.3	2774	2	US-08-643-034A-1	Sequence 1, Appl1	c 222	20.4	28.7	5399	1	US-08-368-071-9	Sequence 9, Appl1
c 150	20.8	29.3	2774	3	US-08-648-650A-1	Sequence 1, Appl1	c 223	20.4	28.7	5399	1	US-08-458-181-9	Sequence 9, Appl1
c 151	20.8	29.3	4454	2	US-08-738-172-2	Sequence 2, Appl1	c 224	20.4	28.7	5399	5	PCT-US93-02172-9	Sequence 9, Appl1
c 152	20.8	29.3	4808	2	US-08-231-193A-10	Sequence 10, Appl1	c 225	20.4	28.7	15872	1	US-09-105-537-1	Sequence 1, Appl1
c 153	20.8	29.3	4808	2	US-08-486-273A-10	Sequence 10, Appl1	c 226	20.4	28.7	20235	1	US-07-642-734C-3	Sequence 3, Appl1
c 154	20.8	29.3	4808	3	US-08-940-086A-10	Sequence 10, Appl1	c 227	20.4	28.7	20235	3	US-08-439-009A-3	Sequence 3, Appl1
c 155	20.8	29.3	4808	4	US-08-940-035A-10	Sequence 10, Appl1	c 228	20.2	28.5	335	4	US-09-439-313-391	Sequence 391, App
c 156	20.6	29.0	1289	2	US-08-344-833-1	Sequence 1, Appl1	c 229	20.2	28.5	619	4	US-08-998-416-842	Sequence 842, App
c 157	20.6	29.0	1820	1	US-08-173-508-7	Sequence 7, Appl1	c 230	20.2	28.5	1401	2	US-08-812-412-1	Sequence 1, Appl1
c 158	20.6	29.0	1821	2	US-08-265-310-7	Sequence 7, Appl1	c 231	20.2	28.5	1401	4	US-09-180-271-4	Sequence 4, Appl1
c 159	20.6	29.0	1821	3	US-08-951-742-7	Sequence 7, Appl1	c 232	20.2	28.5	1434	4	US-09-434-288-3	Sequence 3, Appl1
c 160	20.6	29.0	2681	4	US-08-928-213B-7	Sequence 7, Appl1	c 233	20.2	28.5	1596	1	US-08-716-301-11	Sequence 11, Appl1
c 161	20.6	29.0	2742	3	US-08-911-853-16	Sequence 16, Appl1	c 234	20.2	28.5	1794	4	US-09-232-191-36	Sequence 36, Appl1
c 162	20.6	29.0	2742	4	US-09-479-409-16	Sequence 16, Appl1	c 235	20.2	28.5	1794	4	US-09-232-200-90	Sequence 90, Appl1
c 163	20.6	29.0	2742	4	US-09-479-453-16	Sequence 16, Appl1	c 236	20.2	28.5	1794	4	US-09-232-197-90	Sequence 90, Appl1
c 164	20.6	29.0	3000	4	US-09-192-104-1	Sequence 1, Appl1	c 237	20.2	28.5	1794	4	US-09-232-201-90	Sequence 90, Appl1
c 165	20.6	29.0	3000	4	US-09-543-446-1	Sequence 1, Appl1	c 238	20.2	28.5	1882	1	US-08-696-349-1	Sequence 1, Appl1
c 166	20.6	29.0	3003	4	US-08-915-337-1	Sequence 1, Appl1	c 239	20.2	28.5	1882	5	PCT-US96-13156-1	Sequence 1, Appl1
c 167	20.6	29.0	3013	2	US-09-096-982-6	Sequence 6, Appl1	c 240	20.2	28.5	2007	4	US-09-232-191-22	Sequence 22, Appl1
c 168	20.6	29.0	3013	2	US-08-653-650A-6	Sequence 6, Appl1	c 241	20.2	28.5	2007	4	US-09-232-200-22	Sequence 22, Appl1
c 169	20.6	29.0	3572	2	US-08-713-815A-2	Sequence 2, Appl1	c 242	20.2	28.5	2007	4	US-09-232-197-22	Sequence 22, Appl1
c 170	20.6	29.0	3691	4	US-09-211-704A-3	Sequence 3, Appl1	c 243	20.2	28.5	2077	1	US-09-232-201-22	Sequence 22, Appl1
c 171	20.6	29.0	4848	4	US-08-955-957A-1	Sequence 1, Appl1	c 244	20.2	28.5	2077	1	US-08-217-327-7	Sequence 7, Appl1
c 172	20.6	29.0	4848	4	US-08-955-957A-4	Sequence 4, Appl1	c 245	20.2	28.5	3018	3	US-08-942-572-1	Sequence 1, Appl1
c 173	20.6	29.0	4848	4	US-08-955-957A-6	Sequence 6, Appl1	c 246	20.2	28.5	3279	4	US-09-439-313-382	Sequence 382, App

C 247	20.2	28.5	3411	4	US-08-890-865A-3	Sequence 3, Appli	320	20	28.2	4204	4	US-09-166-448-1	Sequence 1, Appli
248	20.2	28.5	3876	5	PCT-US95-17026-1	Sequence 1, Appli	321	20	28.2	4234	1	US-08-446-038B-1	Sequence 1, Appli
249	20.2	28.5	23673	4	US-09-773-816-1	Sequence 1, Appli	322	20	28.2	4234	1	US-08-446-010B-1	Sequence 1, Appli
C 250	20	28.2	306	4	US-09-199-637A-64	Sequence 64, Appli	323	20	28.2	4234	1	US-08-805-445-1	Sequence 1, Appli
C 251	20	28.2	401	1	US-08-466-033-215	Sequence 215, App	324	20	28.2	4234	1	US-08-064-067D-1	Sequence 1, Appli
C 252	20	28.2	401	1	US-08-444-733-215	Sequence 215, App	325	20	28.2	4234	2	US-09-066-208-1	Sequence 1, Appli
C 253	20	28.2	401	2	US-08-464-134-215	Sequence 215, App	326	20	28.2	4454	2	US-08-738-172-2	Sequence 2, Appli
C 254	20	28.2	401	2	US-08-461-361-215	Sequence 215, App	327	20	28.2	5438	4	US-08-455-200B-5	Sequence 2, Appli
C 255	20	28.2	401	2	US-08-485-910-215	Sequence 215, App	328	20	28.2	8791	5	PCT-US96-01735-5	Sequence 5, Appli
C 256	20	28.2	573	2	US-08-290-665A-110	Sequence 110, App	329	20	28.2	8982	3	US-08-976-253-5	Sequence 5, Appli
C 257	20	28.2	573	5	PCT-US95-10398-110	Sequence 110, App	330	20	28.2	9046	5	US-08-227-536-1	Sequence 5, Appli
258	20	28.2	705	4	US-09-199-637A-60	Sequence 60, Appli	331	20	28.2	9046	5	PCT-US95-04682-1	Sequence 1, Appli
259	20	28.2	721	1	US-08-229-515A-15	Sequence 15, Appli	332	20	28.2	42235	3	US-09-199-637A-60	Sequence 1, Appli
260	20	28.2	721	1	US-08-645-865-15	Sequence 15, Appli	333	20	28.2	49377	3	US-08-766-233A-1	Sequence 1, Appli
261	20	28.2	885	3	US-08-338-368-1	Sequence 1, Appli	C 334	20	28.2	80161	3	US-09-036-987A-1	Sequence 1, Appli
262	20	28.2	1073	1	US-08-356-405-8	Sequence 8, Appli	C 335	20	28.2	80161	4	US-09-370-700-1	Sequence 1, Appli
263	20	28.2	1094	2	US-08-902-294-1	Sequence 1, Appli	336	19.8	27.9	234	4	US-09-189-060B-46	Sequence 4, Appli
264	20	28.2	1094	3	US-09-178-637-1	Sequence 1, Appli	337	19.8	27.9	256	4	US-08-483-533-11	Sequence 11, Appli
265	20	28.2	1178	2	US-08-107-676-26	Sequence 26, Appli	338	19.8	27.9	256	4	US-09-283-471A-11	Sequence 11, Appli
266	20	28.2	1211	2	US-08-107-676-2	Sequence 2, Appli	C 339	19.8	27.9	354	4	US-08-997-457-2	Sequence 14, Appli
C 267	20	28.2	1317	1	US-08-453-472-4	Sequence 4, Appli	340	19.8	27.9	431	4	US-08-483-533-17	Sequence 17, Appli
C 268	20	28.2	1317	1	US-08-038-948-1	Sequence 1, Appli	341	19.8	27.9	431	4	US-09-283-471A-17	Sequence 17, Appli
C 269	20	28.2	1317	1	US-08-453-952-4	Sequence 4, Appli	C 342	19.8	27.9	441	4	US-08-998-416-200	Sequence 20, App
C 270	20	28.2	1317	2	US-08-862-903-4	Sequence 4, Appli	C 343	19.8	27.9	1030	3	US-08-858-003-2	Sequence 2, Appli
C 271	20	28.2	1368	2	US-08-738-172-3	Sequence 3, Appli	C 344	19.8	27.9	1030	3	US-09-078-166-2	Sequence 2, Appli
272	20	28.2	1869	3	US-08-952-967-7	Sequence 7, Appli	C 345	19.8	27.9	1030	3	US-08-997-457-2	Sequence 2, Appli
273	20	28.2	1900	1	US-08-153-848-18	Sequence 18, Appli	346	19.8	27.9	1174	4	US-09-034-985-1	Sequence 2, Appli
274	20	28.2	1900	3	US-09-299-845A-18	Sequence 18, Appli	347	19.8	27.9	1269	3	US-08-265-429A-4	Sequence 1, Appli
275	20	28.2	1900	4	US-09-088-337B-18	Sequence 18, Appli	348	19.8	27.9	1269	5	PCT-US95-09069-4	Sequence 4, Appli
276	20	28.2	1900	5	PCT-US93-11153-18	Sequence 18, Appli	C 349	19.8	27.9	1584	4	US-09-659-166-1	Sequence 1, Appli
277	20	28.2	1947	1	US-07-998-972A-2	Sequence 2, Appli	350	19.8	27.9	1719	4	US-09-047-758A-5	Sequence 5, Appli
278	20	28.2	1947	1	US-08-463-953-2	Sequence 2, Appli	351	19.8	27.9	1724	4	US-09-153-804-8	Sequence 8, Appli
279	20	28.2	1947	1	US-08-462-261-2	Sequence 2, Appli	352	19.8	27.9	1946	4	US-09-029-755C-4	Sequence 4, Appli
280	20	28.2	1947	2	US-08-479-733A-24	Sequence 24, Appli	C 353	19.8	27.9	2130	4	US-08-733-247-5	Sequence 5, Appli
281	20	28.2	1947	3	US-08-487-427-24	Sequence 24, Appli	C 354	19.8	27.9	2142	4	US-08-733-247-8	Sequence 8, Appli
282	20	28.2	1947	3	US-08-479-727A-24	Sequence 24, Appli	C 355	19.8	27.9	2151	1	US-08-477-254A-5	Sequence 5, Appli
283	20	28.2	1947	3	US-08-482-369A-24	Sequence 24, Appli	C 356	19.8	27.9	2151	2	US-08-477-256B-5	Sequence 5, Appli
284	20	28.2	1947	5	PCT-US92-11357-2	Sequence 2, Appli	C 357	19.8	27.9	2151	2	US-08-428-734B-5	Sequence 5, Appli
285	20	28.2	1947	5	PCT-US95-07439-24	Sequence 24, Appli	C 358	19.8	27.9	2151	4	US-08-713-556F-5	Sequence 5, Appli
286	20	28.2	1988	1	US-07-750-080A-15	Sequence 15, Appli	C 359	19.8	27.9	2160	4	US-08-753-247-11	Sequence 11, Appli
287	20	28.2	1988	3	US-08-651-472-15	Sequence 15, Appli	C 360	19.8	27.9	2316	2	US-08-714-677-1	Sequence 1, Appli
288	20	28.2	1988	4	US-08-358-928-15	Sequence 15, Appli	C 361	19.8	27.9	2316	2	US-08-393-540-1	Sequence 1, Appli
289	20	28.2	2058	1	US-08-153-848-6	Sequence 6, Appli	C 362	19.8	27.9	2316	2	US-08-714-537-1	Sequence 1, Appli
290	20	28.2	2058	3	US-09-299-843A-6	Sequence 6, Appli	C 363	19.8	27.9	2385	2	US-07-885-972A-1	Sequence 1, Appli
291	20	28.2	2058	4	US-09-088-337B-6	Sequence 6, Appli	C 364	19.8	27.9	2385	2	US-08-745-880-1	Sequence 1, Appli
292	20	28.2	2058	5	PCT-US93-11153-6	Sequence 6, Appli	C 365	19.8	27.9	2385	2	US-08-480-382-1	Sequence 1, Appli
293	20	28.2	2154	1	US-08-383-750-1	Sequence 1, Appli	C 366	19.8	27.9	2475	4	US-09-624-693A-20	Sequence 20, Appli
294	20	28.2	2154	1	US-08-383-751A-1	Sequence 1, Appli	367	19.8	27.9	2745	1	US-08-363-255-13	Sequence 1, Appli
295	20	28.2	2154	3	US-08-352-678-1	Sequence 1, Appli	368	19.8	27.9	2745	1	US-08-363-255-13	Sequence 1, Appli
296	20	28.2	2154	5	PCT-US93-09636-1	Sequence 1, Appli	C 369	19.8	27.9	2877	4	US-09-029-755C-3	Sequence 3, Appli
297	20	28.2	2160	1	US-08-153-848-14	Sequence 14, Appli	C 370	19.8	27.9	2936	2	US-08-714-677-10	Sequence 10, Appli
298	20	28.2	2160	3	US-09-299-843A-14	Sequence 14, Appli	C 371	19.8	27.9	2936	2	US-08-393-540-10	Sequence 10, Appli
299	20	28.2	2160	4	US-09-088-337B-14	Sequence 14, Appli	C 372	19.8	27.9	2936	2	US-08-714-537-10	Sequence 10, Appli
300	20	28.2	2160	5	PCT-US93-11153-14	Sequence 14, Appli	C 373	19.8	27.9	3061	1	US-09-570-842-1	Sequence 1, Appli
C 301	20	28.2	2310	4	US-09-036-987A-25	Sequence 25, Appli	374	19.8	27.9	3061	1	US-08-700-576-1	Sequence 1, Appli
C 302	20	28.2	2310	4	US-09-370-700-25	Sequence 25, Appli	375	19.8	27.9	3331	4	US-09-047-785A-1	Sequence 1, Appli
C 303	20	28.2	2382	4	US-09-588-256-9	Sequence 9, Appli	376	19.8	27.9	3404	1	US-08-265-429A-1	Sequence 1, Appli
C 304	20	28.2	2600	2	US-08-427-497E-4	Sequence 4, Appli	377	19.8	27.9	3404	5	PCT-US95-09069-1	Sequence 1, Appli
305	20	28.2	2936	2	US-08-738-172-1	Sequence 1, Appli	C 378	19.8	27.9	4200	1	US-07-841-634B-1	Sequence 1, Appli
306	20	28.2	3032	4	US-08-990-140-1	Sequence 1, Appli	C 379	19.8	27.9	4200	1	US-07-946-234A-1	Sequence 1, Appli
307	20	28.2	3032	4	US-09-546-238-1	Sequence 1, Appli	C 380	19.8	27.9	4405	2	US-08-123-161A-1	Sequence 1, Appli
308	20	28.2	3183	4	US-08-427-497E-3	Sequence 3, Appli	C 381	19.8	27.9	4405	4	US-09-485-636-1	Sequence 1, Appli
309	20	28.2	3183	5	PCT-US95-09098-1	Sequence 1, Appli	C 382	19.8	27.9	4405	5	PCT-US93-01560-1	Sequence 1, Appli
310	20	28.2	3429	3	US-08-097-997A-10	Sequence 10, Appli	C 383	19.8	27.9	4405	1	US-07-885-972A-3	Sequence 3, Appli
311	20	28.2	3429	3	US-08-665-574C-10	Sequence 10, Appli	C 384	19.8	27.9	4405	2	US-08-743-880-3	Sequence 3, Appli
312	20	28.2	3429	4	US-08-946-994-10	Sequence 10, Appli	C 385	19.8	27.9	4405	2	US-08-480-382-3	Sequence 3, Appli
C 313	20	28.2	3756	2	US-08-576-626A-1	Sequence 1, Appli	C 386	19.8	27.9	4465	4	US-09-485-636-1	Sequence 1, Appli
314	20	28.2	3774	2	US-08-341-843B-1	Sequence 1, Appli	C 387	19.8	27.9	4465	4	US-09-485-636-1	Sequence 1, Appli
315	20	28.2	3774	2	US-08-427-497E-2	Sequence 2, Appli	388	19.8	27.9	4650	1	US-07-998-003A-102	Sequence 102, App
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319	20	28.2	4204	4	US-09-056-105-6	Sequence 6, Appli	392	19.8	27.9	4650	2	US-08-453-702A-102	Sequence 102, App

393	19.8	27.9	4650	4	US-09-099-639-102	Sequence 102, App	466	19.6	27.6	3044	3	US-09-139-491-44	Sequence 44, App1
394	19.8	27.9	4650	5	PCT-US93-12588-102	Sequence 102, App	467	19.6	27.6	3044	2	PCT-US92-03222-44	Sequence 44, App1
395	19.8	27.9	4650	5	PCT-US95-08071-102	Sequence 102, App	468	19.6	27.6	3382	5	US-08-682-847-1	Sequence 1, App1
396	19.8	27.9	4655	2	US-08-231-193A-57	Sequence 57, App1	469	19.6	27.6	3519	1	US-08-035-558-1	Sequence 1, App1
397	19.8	27.9	4655	2	US-08-486-273A-57	Sequence 57, App1	470	19.6	27.6	3789	1	US-07-872-644A-42	Sequence 42, App1
398	19.8	27.9	4655	3	US-08-940-086A-57	Sequence 57, App1	471	19.6	27.6	3789	1	US-08-297-494A-42	Sequence 42, App1
399	19.8	27.9	4695	4	US-08-940-035A-57	Sequence 57, App1	472	19.6	27.6	3789	1	US-08-297-510A-42	Sequence 42, App1
400	19.8	27.9	4707	3	US-09-181-706-1	Sequence 1, App1	473	19.6	27.6	3789	1	US-08-479-532A-42	Sequence 42, App1
401	19.8	27.9	4707	4	US-09-459-066-1	Sequence 1, App1	474	19.6	27.6	3789	1	US-08-455-526A-42	Sequence 42, App1
402	19.8	27.9	4707	4	US-09-459-066-1	Sequence 1, App1	475	19.6	27.6	3789	1	US-08-455-526A-42	Sequence 42, App1
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406	19.8	27.9	5538	3	US-08-940-086A-55	Sequence 55, App1	479	19.6	27.6	4131	1	US-08-297-494A-38	Sequence 38, App1
407	19.8	27.9	5538	4	US-08-940-035A-55	Sequence 55, App1	480	19.6	27.6	4131	1	US-08-297-510A-38	Sequence 38, App1
408	19.8	27.9	5605	4	US-09-268-140-6	Sequence 6, App1	481	19.6	27.6	4131	1	US-08-479-532A-38	Sequence 38, App1
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411	19.8	27.9	8252	1	US-08-393-703-15	Sequence 15, App1	484	19.6	27.6	4131	5	US-09-139-491A-38	Sequence 38, App1
412	19.8	27.9	8252	5	PCT-US93-11721-15	Sequence 15, App1	485	19.6	27.6	4131	5	PCT-US92-03222-38	Sequence 38, App1
413	19.8	27.9	9785	4	US-09-479-128-1	Sequence 1, App1	486	19.6	27.6	4425	1	US-08-222-616-32	Sequence 32, App1
414	19.8	27.9	30001	1	US-08-125-468-1	Sequence 1, App1	487	19.6	27.6	4425	5	PCT-US95-04228-32	Sequence 32, App1
415	19.8	27.9	30001	2	US-08-474-933-1	Sequence 1, App1	488	19.6	27.6	4425	3	US-08-717-294A-42	Sequence 42, App1
416	19.6	27.6	207	4	US-08-990-823-24	Sequence 24, App1	489	19.6	27.6	4758	3	US-09-191-647-1	Sequence 1, App1
417	19.6	27.6	471	2	US-08-883-070-2	Sequence 2, App1	490	19.6	27.6	4758	4	US-09-540-745A-1	Sequence 1, App1
418	19.6	27.6	484	5	PCT-US95-08295-16	Sequence 16, App1	491	19.6	27.6	4758	4	US-09-540-745A-1	Sequence 1, App1
419	19.6	27.6	561	5	PCT-US95-06726-35	Sequence 35, App1	492	19.6	27.6	5996	3	US-09-028-934A-33	Sequence 33, App1
420	19.6	27.6	798	3	US-09-354-129-5	Sequence 5, App1	493	19.6	27.6	7676	2	US-08-451-778A-7	Sequence 7, App1
421	19.6	27.6	831	4	US-08-836-075A-65	Sequence 65, App1	494	19.6	27.6	7676	2	US-08-451-778A-7	Sequence 7, App1
422	19.6	27.6	969	2	US-08-700-637-1	Sequence 1, App1	495	19.6	27.6	7676	5	US-08-998-208-7	Sequence 7, App1
423	19.6	27.6	975	4	US-09-365-150-3	Sequence 3, App1	496	19.6	27.6	7676	5	PCT-US95-06743-7	Sequence 7, App1
424	19.6	27.6	1073	4	US-09-430-503-25	Sequence 25, App1	497	19.6	27.6	71989	4	US-09-443-501A-2	Sequence 2, App1
425	19.6	27.6	1073	4	US-09-430-503-25	Sequence 25, App1	498	19.4	27.3	210	6	5212296-19	Patent No. 5212296
426	19.6	27.6	1073	4	US-09-430-503-29	Sequence 29, App1	499	19.4	27.3	217	4	US-09-060-756-558	Sequence 58, App
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430	19.6	27.6	1330	3	US-08-888-077A-26	Sequence 26, App1	503	19.4	27.3	491	4	US-09-060-852A-8	Sequence 8, App1
431	19.6	27.6	1371	3	US-08-462-969A-1	Sequence 1, App1	504	19.4	27.3	640	2	US-08-403-8520-17	Sequence 17, App1
432	19.6	27.6	1576	6	5260432-1	Patent No. 5260432	505	19.4	27.3	640	4	US-08-510-646B-8	Sequence 8, App1
433	19.6	27.6	1679	4	US-09-069-023-35	Sequence 35, App1	506	19.4	27.3	640	4	US-09-231-818A-8	Sequence 8, App1
434	19.6	27.6	1753	2	US-08-750-134A-8	Sequence 8, App1	507	19.4	27.3	669	2	US-08-820-170A-17	Sequence 17, App1
435	19.6	27.6	1753	2	US-09-363-745-8	Sequence 8, App1	508	19.4	27.3	669	3	US-09-055-699-17	Sequence 17, App1
436	19.6	27.6	1844	2	US-08-538-816A-10	Sequence 10, App1	509	19.4	27.3	669	4	US-09-273-565-17	Sequence 17, App1
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441	19.6	27.6	1894	2	US-09-208-394-8	Sequence 8, App1	514	19.4	27.3	830	4	US-08-913-362A-5	Sequence 5, App1
442	19.6	27.6	1977	4	US-09-227-357-83	Sequence 83, App1	515	19.4	27.3	888	4	US-09-199-637A-340	Sequence 340, App
443	19.6	27.6	2207	4	US-08-858-207A-46	Sequence 46, App1	516	19.4	27.3	1128	2	US-08-820-170A-18	Sequence 18, App1
444	19.6	27.6	2541	2	US-08-656-393-1	Sequence 1, App1	517	19.4	27.3	1128	3	US-09-055-699-18	Sequence 18, App1
445	19.6	27.6	2550	1	US-08-245-295-10	Sequence 10, App1	518	19.4	27.3	1128	4	US-09-273-565-18	Sequence 18, App1
446	19.6	27.6	2550	1	US-08-481-130-10	Sequence 10, App1	519	19.4	27.3	1128	4	US-09-565-538A-18	Sequence 18, App1
447	19.6	27.6	2550	1	US-08-656-984A-10	Sequence 10, App1	520	19.4	27.3	1128	4	US-09-565-538A-18	Sequence 18, App1
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450	19.6	27.6	2550	2	US-09-305-640-1	Sequence 1, App1	523	19.4	27.3	1344	4	US-09-199-637A-350	Sequence 350, App
451	19.6	27.6	2675	2	US-08-883-070-1	Sequence 1, App1	524	19.4	27.3	1459	2	US-08-824-707-1	Sequence 1, App1
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463	19.6	27.6	3044	1	US-08-479-532A-44	Sequence 44, App1	536	19.4	27.3	1981	3	US-09-017-706A-5	Sequence 5, App1
464	19.6	27.6	3044	1	US-08-455-526A-44	Sequence 44, App1	537	19.4	27.3	1981	3	US-09-017-706A-6	Sequence 6, App1
465	19.6	27.6	3044	1	US-08-455-525A-44	Sequence 44, App1	538	19.4	27.3	1981	3	US-09-017-706A-7	Sequence 7, App1

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C 542	19.4	27.3	2406	1	US-07-689-008-4	Sequence 4, Appli	615	19.2	27.0	350	2	US-09-036-089-2	Sequence 2, Appli
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544	19.4	27.3	2520	2	US-08-450-351-3	Sequence 3, Appli	617	19.2	27.0	485	2	US-08-403-852D-15	Sequence 15, Appli
545	19.4	27.3	2582	2	US-08-816-105A-2	Sequence 2, Appli	618	19.2	27.0	485	3	US-08-510-646B-15	Sequence 15, Appli
546	19.4	27.3	3014	2	US-08-629-939-1	Sequence 1, Appli	619	19.2	27.0	485	4	US-09-231-818-15	Sequence 15, Appli
547	19.4	27.3	3014	1	US-08-759-873-1	Sequence 1, Appli	620	19.2	27.0	485	4	US-09-085-199B-32	Sequence 32, Appli
548	19.4	27.3	3468	1	US-07-951-715A-2	Sequence 2, Appli	C 621	19.2	27.0	530	3	US-08-758-662-4	Sequence 4, Appli
549	19.4	27.3	3468	1	US-07-951-715A-4	Sequence 4, Appli	C 622	19.2	27.0	549	3	US-08-441-971-58	Sequence 58, Appli
550	19.4	27.3	3468	1	US-07-951-715A-8	Sequence 8, Appli	C 623	19.2	27.0	549	3	US-08-441-971-59	Sequence 59, Appli
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553	19.4	27.3	3468	2	US-08-459-448A-8	Sequence 8, Appli	C 626	19.2	27.0	549	4	US-08-221-653-59	Sequence 59, Appli
554	19.4	27.3	3468	3	US-08-459-555A-2	Sequence 2, Appli	C 627	19.2	27.0	549	4	US-08-221-653-60	Sequence 60, Appli
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556	19.4	27.3	3468	3	US-08-459-555A-8	Sequence 8, Appli	C 629	19.2	27.0	549	4	US-08-442-144A-59	Sequence 59, Appli
557	19.4	27.3	3468	3	US-08-459-504B-2	Sequence 2, Appli	C 630	19.2	27.0	549	4	US-08-442-144A-60	Sequence 60, Appli
558	19.4	27.3	3468	3	US-08-459-504B-4	Sequence 4, Appli	C 631	19.2	27.0	549	4	US-08-441-970-58	Sequence 58, Appli
559	19.4	27.3	3468	3	US-08-459-504B-8	Sequence 8, Appli	C 632	19.2	27.0	549	4	US-08-441-970-59	Sequence 59, Appli
560	19.4	27.3	3468	3	US-08-459-444-2	Sequence 2, Appli	C 633	19.2	27.0	549	4	US-08-441-970-60	Sequence 60, Appli
561	19.4	27.3	3468	3	US-08-459-444-4	Sequence 4, Appli	C 634	19.2	27.0	573	2	US-08-290-665A-109	Sequence 109, App
562	19.4	27.3	3468	3	US-08-459-444-8	Sequence 8, Appli	C 635	19.2	27.0	573	2	US-08-290-665A-113	Sequence 113, App
563	19.4	27.3	3468	3	US-09-053-549-3	Sequence 3, Appli	C 636	19.2	27.0	573	2	US-08-290-665A-115	Sequence 115, App
564	19.4	27.3	3468	3	US-09-053-549-5	Sequence 5, Appli	C 637	19.2	27.0	573	5	PCT-US95-10398-109	Sequence 109, App
565	19.4	27.3	3468	4	US-09-547-422-2	Sequence 2, Appli	C 638	19.2	27.0	573	5	PCT-US95-10398-113	Sequence 113, App
566	19.4	27.3	3468	4	US-09-547-422-4	Sequence 4, Appli	C 639	19.2	27.0	757	5	PCT-US95-10398-115	Sequence 115, App
567	19.4	27.3	3468	4	US-09-547-422-8	Sequence 8, Appli	C 640	19.2	27.0	757	1	US-08-229-519A-10	Sequence 10, Appli
568	19.4	27.3	3546	1	US-07-951-715A-27	Sequence 27, Appli	641	19.2	27.0	757	1	US-08-645-865-10	Sequence 10, Appli
569	19.4	27.3	3546	2	US-08-459-448A-27	Sequence 27, Appli	C 642	19.2	27.0	834	4	US-08-191-160-5	Sequence 5, Appli
570	19.4	27.3	3546	2	US-08-459-595A-27	Sequence 27, Appli	C 643	19.2	27.0	834	2	US-08-935-450-10	Sequence 10, Appli
571	19.4	27.3	3546	3	US-08-459-504B-27	Sequence 27, Appli	C 644	19.2	27.0	1037	2	US-08-462-195-3	Sequence 3, Appli
572	19.4	27.3	3546	3	US-08-459-444-27	Sequence 27, Appli	C 645	19.2	27.0	1037	2	US-08-636-883-3	Sequence 3, Appli
573	19.4	27.3	3546	4	US-09-547-422-27	Sequence 27, Appli	C 646	19.2	27.0	1037	3	US-09-127-897-9	Sequence 9, Appli
574	19.4	27.3	3547	1	US-07-951-715A-16	Sequence 16, Appli	C 647	19.2	27.0	1167	1	US-08-324-977-3	Sequence 3, Appli
575	19.4	27.3	3547	2	US-08-459-448A-16	Sequence 16, Appli	C 648	19.2	27.0	1167	2	US-08-384-616-9	Sequence 9, Appli
576	19.4	27.3	3547	3	US-08-459-595A-16	Sequence 16, Appli	C 649	19.2	27.0	1167	4	US-08-904-666A-9	Sequence 9, Appli
577	19.4	27.3	3547	3	US-08-459-504B-16	Sequence 16, Appli	C 650	19.2	27.0	1167	2	US-09-315-850-9	Sequence 9, Appli
578	19.4	27.3	3547	3	US-08-459-444-16	Sequence 16, Appli	C 651	19.2	27.0	1260	4	US-08-949-202-1	Sequence 1, Appli
579	19.4	27.3	3547	4	US-09-547-422-16	Sequence 16, Appli	652	19.2	27.0	1260	4	US-09-418-175-1	Sequence 1, Appli
580	19.4	27.3	3708	2	US-08-680-376-29	Sequence 29, Appli	653	19.2	27.0	1346	3	US-08-949-202-3	Sequence 3, Appli
581	19.4	27.3	4287	1	US-08-244-189-1	Sequence 1, Appli	654	19.2	27.0	1346	4	US-09-418-175-3	Sequence 3, Appli
582	19.4	27.3	4287	1	US-08-306-691B-53	Sequence 53, Appli	C 655	19.2	27.0	1499	2	US-08-324-977-3	Sequence 3, Appli
583	19.4	27.3	4488	4	US-08-406-030A-3	Sequence 3, Appli	C 656	19.2	27.0	1499	2	US-08-384-616-3	Sequence 3, Appli
584	19.4	27.3	4488	6	US-08-406-030A-3	Sequence 3, Appli	C 657	19.2	27.0	1499	2	US-08-904-666A-9	Sequence 9, Appli
C 585	19.4	27.3	5036	4	US-09-177-349-2	Sequence 2, Appli	C 658	19.2	27.0	1499	4	US-09-315-850-3	Sequence 3, Appli
C 586	19.4	27.3	5467	1	US-07-745-206A-12	Sequence 12, Appli	C 659	19.2	27.0	1539	4	US-08-470-426B-17	Sequence 17, Appli
C 587	19.4	27.3	5467	2	US-08-311-363-12	Sequence 12, Appli	660	19.2	27.0	1571	4	US-08-866-435-32	Sequence 32, Appli
588	19.4	27.3	6441	4	US-08-669-785-1	Sequence 1, Appli	661	19.2	27.0	1571	4	US-08-744-231-32	Sequence 32, Appli
C 589	19.4	27.3	6443	6	5183745-5	Patent No. 5183745	662	19.2	27.0	1618	2	US-08-533-669A-9	Sequence 9, Appli
C 590	19.4	27.3	7175	1	US-08-455-543A-8	Sequence 8, Appli	663	19.2	27.0	1618	2	US-08-607-509-1	Sequence 1, Appli
C 591	19.4	27.3	7175	2	US-08-193-078B-8	Sequence 8, Appli	664	19.2	27.0	1618	2	US-08-454-036-1	Sequence 1, Appli
C 592	19.4	27.3	7175	2	US-08-223-305C-8	Sequence 8, Appli	665	19.2	27.0	1618	2	US-08-638-642-1	Sequence 1, Appli
C 593	19.4	27.3	7175	2	US-08-149-037D-8	Sequence 8, Appli	666	19.2	27.0	1618	5	US-08-989-370-1	Sequence 1, Appli
C 594	19.4	27.3	7175	3	US-08-949-386-8	Sequence 8, Appli	667	19.2	27.0	1618	5	PCT-US95-05064-1	Sequence 1, Appli
C 595	19.4	27.3	7175	4	US-08-450-562-8	Sequence 8, Appli	668	19.2	27.0	1680	1	US-08-014-723-13	Sequence 13, Appli
C 596	19.4	27.3	7362	1	US-08-984-709A-8	Sequence 8, Appli	C 669	19.2	27.0	1680	1	US-08-014-723-15	Sequence 15, Appli
C 597	19.4	27.3	7362	1	US-08-455-543A-7	Sequence 7, Appli	C 670	19.2	27.0	1680	1	US-08-110-011A-13	Sequence 13, Appli
C 598	19.4	27.3	7362	2	US-08-193-078B-7	Sequence 7, Appli	C 671	19.2	27.0	1680	1	US-08-110-011A-15	Sequence 15, Appli
C 599	19.4	27.3	7362	2	US-08-223-305C-7	Sequence 7, Appli	C 672	19.2	27.0	1734	6	5352575-8	Patent No. 5352575
C 600	19.4	27.3	7362	2	US-08-149-037D-7	Sequence 7, Appli	C 673	19.2	27.0	1758	4	US-09-191-171-6	Sequence 6, Appli
C 601	19.4	27.3	7362	2	US-08-949-386-7	Sequence 7, Appli	C 674	19.2	27.0	1801	5	US-09-385-707-6	Sequence 6, Appli
C 602	19.4	27.3	7362	3	US-08-450-562-7	Sequence 7, Appli	C 675	19.2	27.0	1801	5	PCT-US95-02455-1	Sequence 1, Appli
C 603	19.4	27.3	7362	4	US-08-984-709A-7	Sequence 7, Appli	C 676	19.2	27.0	1863	2	US-08-470-426B-14	Sequence 14, Appli
C 604	19.4	27.3	9540	1	US-07-689-008-1	Sequence 1, Appli	C 677	19.2	27.0	2116	4	US-08-191-160-21	Sequence 21, Appli
C 605	19.4	27.3	13987	2	US-08-804-227C-13	Sequence 13, Appli	C 678	19.2	27.0	2210	4	US-08-464-700-33	Sequence 33, Appli
C 606	19.4	27.3	15297	4	US-09-817-180-3	Sequence 3, Appli	C 679	19.2	27.0	2242	4	US-08-641-627A-37	Sequence 37, Appli
C 607	19.4	27.3	16836	4	US-09-147-236-1	Sequence 1, Appli	C 680	19.2	27.0	2427	2	US-08-678-039A-39	Sequence 39, Appli
C 608	19.4	27.3	16836	4	US-09-147-236-10	Sequence 10, Appli	681	19.2	27.0	2561	4	US-09-416-221-7	Sequence 7, Appli
C 609	19.4	27.3	44377	2	US-08-804-227C-7	Sequence 7, Appli	C 682	19.2	27.0	2952	2	US-09-318-794A-4	Sequence 4, Appli
C 610	19.4	27.3	44377	2	US-08-804-198-1	Sequence 1, Appli	C 683	19.2	27.0	3107	2	US-08-813-940-3	Sequence 3, Appli
C 611	19.2	27.0	298	2	US-09-036-089-4	Sequence 4, Appli	C 684	19.2	27.0	3590	1	US-08-587-889-1	Sequence 1, Appli

C 685	19.2	27.0	3590	5	PCT-US96-09193-1	Sequence 1, Appl1	758	19	26.8	1422	4	US-08-979-608A-13	Sequence 13, Appl1
686	19.2	27.0	4473	2	US-09-048-804-1	Sequence 1, Appl1	C 759	19	26.8	1456	3	US-09-037-135-1	Sequence 1, Appl1
687	19.2	27.0	4473	4	US-09-056-105-26	Sequence 26, Appl1	760	19	26.8	1554	1	US-08-045-269C-1	Sequence 1, Appl1
688	19.2	27.0	4524	2	US-08-845-998-7	Sequence 7, Appl1	761	19	26.8	1554	3	US-08-371-680-1	Sequence 1, Appl1
689	19.2	27.0	4524	3	US-09-206-537-7	Sequence 7, Appl1	762	19	26.8	1554	5	PCT-US84-01198-1	Sequence 1, Appl1
690	19.2	27.0	4524	4	US-09-430-854-7	Sequence 7, Appl1	763	19	26.8	1617	4	US-08-979-608A-11	Sequence 11, Appl1
691	19.2	27.0	4530	1	US-08-229-515A-9	Sequence 9, Appl1	764	19	26.8	1828	4	US-09-153-804-3	Sequence 3, Appl1
692	19.2	27.0	4530	1	US-08-645-865-9	Sequence 9, Appl1	765	19	26.8	1839	4	US-09-516-914-6	Sequence 6, Appl1
693	19.2	27.0	4837	1	US-09-629-616-1	Sequence 1, Appl1	766	19	26.8	1862	3	US-08-999-723-1	Sequence 1, Appl1
C 694	19.2	27.0	5455	1	US-08-342-930-1	Sequence 1, Appl1	767	19	26.8	1862	4	US-09-434-427-1	Sequence 1, Appl1
C 695	19.2	27.0	6039	1	US-08-324-977-11	Sequence 11, Appl1	C 768	19	26.8	1933	3	US-08-974-380-1	Sequence 1, Appl1
C 696	19.2	27.0	6039	2	US-08-384-616-11	Sequence 11, Appl1	769	19	26.8	2037	2	US-08-535-276-1	Sequence 1, Appl1
C 697	19.2	27.0	6039	2	US-08-904-686A-11	Sequence 11, Appl1	770	19	26.8	2138	3	US-08-776-271-1	Sequence 1, Appl1
C 698	19.2	27.0	6039	4	US-09-315-850-11	Sequence 11, Appl1	771	19	26.8	2138	3	US-09-215-035-1	Sequence 1, Appl1
699	19.2	27.0	6503	4	US-09-404-650-12	Sequence 12, Appl1	772	19	26.8	2267	4	US-08-679-645-25	Sequence 25, Appl1
C 700	19.2	27.0	6709	4	US-09-285-601-3	Sequence 3, Appl1	C 773	19	26.8	2278	1	US-08-258-188-1	Sequence 1, Appl1
C 701	19.2	27.0	9030	1	US-08-324-977-13	Sequence 13, Appl1	C 774	19	26.8	2278	1	US-08-526-813-1	Sequence 1, Appl1
C 702	19.2	27.0	9030	2	US-08-384-616-13	Sequence 13, Appl1	C 775	19	26.8	2278	5	PCT-US95-08554-1	Sequence 1, Appl1
C 703	19.2	27.0	9030	2	US-08-904-686A-13	Sequence 13, Appl1	776	19	26.8	2588	2	US-08-796-414B-6	Sequence 6, Appl1
C 704	19.2	27.0	9030	4	US-09-315-850-13	Sequence 13, Appl1	C 777	19	26.8	2936	2	US-08-738-172-1	Sequence 1, Appl1
C 705	19.2	27.0	9058	4	US-08-913-014A-9	Sequence 9, Appl1	778	19	26.8	3810	2	US-08-475-844-8	Sequence 8, Appl1
C 706	19.2	27.0	9416	2	US-08-324-977-1	Sequence 1, Appl1	779	19	26.8	3810	5	PCT-US95-08429-8	Sequence 8, Appl1
C 707	19.2	27.0	9416	2	US-08-384-616-1	Sequence 1, Appl1	780	19	26.8	4425	1	US-08-222-616-32	Sequence 32, Appl1
C 708	19.2	27.0	9416	2	US-08-904-686A-1	Sequence 1, Appl1	781	19	26.8	4425	5	PCT-US95-04228-32	Sequence 32, Appl1
C 709	19.2	27.0	9416	4	US-09-315-850-1	Sequence 1, Appl1	782	19	26.8	4496	4	US-08-765-907A-6	Sequence 6, Appl1
C 710	19.2	27.0	9595	3	US-09-014-416-4	Sequence 4, Appl1	C 783	19	26.8	5437	1	US-07-661-610C-1	Sequence 1, Appl1
C 711	19.2	27.0	9599	3	US-09-014-416-6	Sequence 6, Appl1	C 784	19	26.8	5515	4	US-09-398-193-98	Sequence 98, Appl1
C 712	19.2	27.0	13987	2	US-08-804-227C-13	Sequence 13, Appl1	785	19	26.8	5595	1	US-08-920-817-23	Sequence 23, Appl1
713	19.2	27.0	14272	4	US-09-516-914-23	Sequence 23, Appl1	786	19	26.8	5975	1	US-08-920-827-23	Sequence 23, Appl1
714	19.2	27.0	36741	4	US-09-301-665-3	Sequence 3, Appl1	787	19	26.8	5975	1	US-08-921-177-23	Sequence 23, Appl1
C 715	19.2	27.0	44377	2	US-08-804-227C-7	Sequence 7, Appl1	788	19	26.8	5975	1	US-08-362-577C-23	Sequence 23, Appl1
C 716	19.2	27.0	44377	2	US-08-804-198-1	Sequence 1, Appl1	789	19	26.8	5975	2	US-08-920-828-23	Sequence 23, Appl1
717	19.2	27.0	49377	1	US-08-764-233A-1	Sequence 1, Appl1	790	19	26.8	6235	4	US-09-305-384-5	Sequence 5, Appl1
C 718	19.2	27.0	68750	3	US-09-335-409-1	Sequence 1, Appl1	791	19	26.8	6529	4	US-08-789-392C-1	Sequence 1, Appl1
C 719	19.2	27.0	68750	4	US-09-568-102-1	Sequence 1, Appl1	792	19	26.8	6679	4	US-09-305-384-1	Sequence 1, Appl1
C 720	19.2	27.0	68750	4	US-09-567-96A-1	Sequence 1, Appl1	793	19	26.8	6911	1	US-08-311-174-4	Sequence 4, Appl1
C 721	19.2	27.0	68750	4	US-09-568-480-1	Sequence 1, Appl1	794	19	26.8	7824	4	US-08-718-388-6	Sequence 6, Appl1
C 722	19.2	27.0	68750	4	US-09-568-486-1	Sequence 1, Appl1	795	19	26.8	8201	1	US-08-253-155A-9	Sequence 9, Appl1
C 723	19.2	27.0	68750	4	US-09-568-472-1	Sequence 1, Appl1	C 796	19	26.8	9661	4	US-08-934-386-7	Sequence 7, Appl1
724	19.2	26.8	231	4	US-09-439-313-459	Sequence 459, App	C 797	19	26.8	10095	3	US-08-822-586-45	Sequence 45, Appl1
725	19.2	26.8	248	4	US-09-007-005-32	Sequence 32, Appl1	C 798	19	26.8	10763	2	US-08-977-306-1	Sequence 1, Appl1
726	19.2	26.8	248	4	US-09-244-796-32	Sequence 32, Appl1	C 799	19	26.8	10763	2	US-08-977-306-1	Sequence 1, Appl1
727	19.2	26.8	277	4	US-09-007-005-3	Sequence 3, Appl1	C 800	19	26.8	11558	4	US-09-134-246-8	Sequence 8, Appl1
728	19.2	26.8	277	4	US-09-244-796-3	Sequence 3, Appl1	C 801	19	26.8	13842	4	US-09-105-537-30	Sequence 30, Appl1
C 729	19.2	26.8	705	4	US-08-998-416-1059	Sequence 1059, Ap	C 802	19	26.8	16382	4	US-08-718-388-7	Sequence 8, Appl1
730	19.2	26.8	806	3	US-09-154-083-7	Sequence 7, Appl1	803	19	26.8	35060	3	US-08-814-095-7	Sequence 7, Appl1
731	19.2	26.8	1010	4	US-08-991-789A-5	Sequence 5, Appl1	C 804	19	26.8	38778	4	US-09-105-537-5	Sequence 5, Appl1
732	19.2	26.8	1010	4	US-09-062-451-5	Sequence 5, Appl1	C 805	19	26.8	38778	3	US-09-320-878-19	Sequence 19, Appl1
733	19.2	26.8	1074	1	US-08-045-269C-3	Sequence 3, Appl1	806	19	26.8	50341	1	US-08-247-901C-1	Sequence 1, Appl1
734	19.2	26.8	1074	3	US-08-371-680-3	Sequence 3, Appl1	807	19	26.8	50341	2	US-09-075-904-1	Sequence 1, Appl1
735	19.2	26.8	1074	5	PCT-US94-01198-3	Sequence 3, Appl1	808	19	26.8	52297	4	US-09-426-436-1	Sequence 1, Appl1
736	19.2	26.8	1080	3	US-09-043-627-1	Sequence 1, Appl1	809	19	26.8	52297	4	US-08-705-557-1	Sequence 1, Appl1
737	19.2	26.8	1194	4	US-08-765-907A-9	Sequence 9, Appl1	810	19	26.8	97	4	US-08-210-222-11	Sequence 11, Appl1
738	19.2	26.8	1248	4	US-09-232-200-54	Sequence 54, Appl1	811	18.8	26.5	236	4	US-09-060-756-209	Sequence 209, App
739	19.2	26.8	1248	4	US-09-232-197-54	Sequence 54, Appl1	812	18.8	26.5	375	4	US-08-981-189B-16	Sequence 16, Appl1
740	19.2	26.8	1248	4	US-09-232-201-54	Sequence 54, Appl1	813	18.8	26.5	398	4	US-09-086-483A-15	Sequence 15, Appl1
741	19.2	26.8	1252	4	US-09-305-384-7	Sequence 7, Appl1	814	18.8	26.5	461	2	US-08-821-009-2	Sequence 2, Appl1
742	19.2	26.8	1278	4	US-09-232-191-18	Sequence 18, Appl1	815	18.8	26.5	461	2	US-09-099-572-2	Sequence 2, Appl1
743	19.2	26.8	1278	4	US-09-232-200-18	Sequence 18, Appl1	C 816	18.8	26.5	541	4	US-09-134-246-7	Sequence 4, Appl1
744	19.2	26.8	1278	4	US-09-232-197-18	Sequence 18, Appl1	817	18.8	26.5	603	4	US-08-918-112-141	Sequence 141, App
745	19.2	26.8	1278	4	US-09-232-201-18	Sequence 18, Appl1	818	18.8	26.5	603	4	US-08-918-112-141	Sequence 141, App
C 746	19.2	26.8	1299	1	US-07-661-610C-11	Sequence 11, Appl1	819	18.8	26.5	650	4	US-08-461-052-5	Sequence 5, Appl1
747	19.2	26.8	1336	4	US-08-718-388-2	Sequence 2, Appl1	820	18.8	26.5	650	4	US-08-689-411-5	Sequence 5, Appl1
748	19.2	26.8	1352	1	US-08-233-609-2	Sequence 2, Appl1	821	18.8	26.5	655	4	US-08-818-112-136	Sequence 136, App
749	19.2	26.8	1352	1	US-08-444-083-2	Sequence 2, Appl1	822	18.8	26.5	655	4	US-08-818-112-136	Sequence 136, App
750	19.2	26.8	1352	1	US-08-286-304-2	Sequence 2, Appl1	823	18.8	26.5	655	4	US-09-056-556-141	Sequence 141, App
751	19.2	26.8	1352	1	US-08-442-745-2	Sequence 2, Appl1	824	18.8	26.5	662	4	US-09-129-030-41	Sequence 41, Appl1
752	19.2	26.8	1352	1	US-08-443-129-2	Sequence 2, Appl1	C 825	18.8	26.5	664	4	US-09-328-111-279	Sequence 279, App
753	19.2	26.8	1352	1	US-08-443-952-2	Sequence 2, Appl1	826	18.8	26.5	712	2	US-08-747-536-3	Sequence 3, Appl1
754	19.2	26.8	1352	1	US-08-443-130-2	Sequence 2, Appl1	827	18.8	26.5	712	2	US-08-747-536-3	Sequence 3, Appl1
755	19.2	26.8	1352	3	US-08-898-911-2	Sequence 2, Appl1	828	18.8	26.5	722	2	US-08-747-536-7	Sequence 7, Appl1
756	19.2	26.8	1352	5	PCT-US95-04467-2	Sequence 5, Appl1	829	18.8	26.5	787	1	US-08-702-609A-1	Sequence 1, Appl1
757	19.2	26.8	1362	4	US-08-979-608A-12	Sequence 12, Appl1	830	18.8	26.5	816	3	US-08-545-809A-14	Sequence 14, Appl1

831	18.8	26.5	1024	6	5169835-16	Patent No. 5169835	904	18.8	26.5	6256	2	US-08-587-680A-1	Sequence 1, Appl1
832	18.8	26.5	1071	2	US-08-997-080-180	Sequence 180, App	C 905	18.8	26.5	6756	1	US-08-151-574-31	Sequence 31, Appl1
833	18.8	26.5	1071	2	US-08-997-362-180	Sequence 180, App	C 906	18.8	26.5	6756	2	US-08-419-448-31	Sequence 31, Appl1
834	18.8	26.5	1071	4	US-09-095-855-180	Sequence 180, App	C 907	18.8	26.5	6756	4	US-09-233-510-31	Sequence 31, Appl1
835	18.8	26.5	1071	4	US-09-324-542-180	Sequence 180, App	C 908	18.8	26.5	8460	1	US-08-469-005A-9	Sequence 9, Appl1
836	18.8	26.5	1080	2	US-09-205-922-1	Sequence 1, Appl1	C 909	18.8	26.5	8519	4	US-09-261-907-1	Sequence 1, Appl1
837	18.8	26.5	1212	6	5212296-17	Patent No. 5212296	C 910	18.8	26.5	9540	1	US-07-689-008-1	Sequence 1, Appl1
838	18.8	26.5	1217	2	US-08-846-762-100	Sequence 100, App	C 911	18.8	26.5	11495	4	US-09-056-105-9	Sequence 9, Appl1
839	18.8	26.5	1339	3	US-08-468-856B-3	Sequence 3, Appl1	C 912	18.8	26.5	11958	4	US-09-134-246-8	Sequence 8, Appl1
840	18.8	26.5	1339	3	US-08-468-859A-6	Sequence 3, Appl1	C 913	18.8	26.5	12412	1	US-08-390-878-18	Sequence 18, Appl1
841	18.8	26.5	1345	1	US-08-362-670B-33	Sequence 33, Appl	C 914	18.8	26.5	16885	1	US-08-390-878-16	Sequence 16, Appl
842	18.8	26.5	1345	3	US-08-333-576C-33	Sequence 33, Appl	C 915	18.8	26.5	35100	2	US-08-770-379-19	Sequence 19, Appl
843	18.8	26.5	1345	4	US-08-808-324-33	Sequence 33, Appl	C 916	18.8	26.5	35100	4	US-08-757-669A-19	Sequence 19, Appl
844	18.8	26.5	1345	5	PCT-US94-14030A-33	Sequence 33, Appl	C 917	18.8	26.5	35100	4	US-09-230-371A-19	Sequence 19, Appl
C 845	18.8	26.5	1443	3	US-08-959-381A-3	Sequence 3, Appl1	C 918	18.8	26.5	36519	3	US-08-923-137-2	Sequence 2, Appl1
846	18.8	26.5	1473	2	US-08-602-725-31	Sequence 31, Appl	C 919	18.8	26.5	49272	1	US-08-614-770A-1	Sequence 1, Appl1
847	18.8	26.5	1487	3	US-08-702-609A-3	Sequence 3, Appl1	C 920	18.6	26.2	69	5	PCT-US94-06079-36	Sequence 36, Appl1
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850	18.8	26.5	1535	4	US-08-461-002-1	Sequence 1, Appl1	C 923	18.6	26.2	405	4	US-09-060-756-675	Sequence 675, App
851	18.8	26.5	1535	5	US-08-689-411-1	Sequence 1, Appl1	C 924	18.6	26.2	414	3	US-08-804-180C-1	Sequence 1, Appl1
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878	18.8	26.5	2874	4	US-08-702-609A-5	Sequence 5, Appl1	C 951	18.6	26.2	1021	2	US-08-889-666-17	Sequence 17, App
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; APPLICANT: Uhl, George R.
; APPLICANT: Wang, Jia-Bel
; APPLICANT: Johnson, Peter S.
; APPLICANT: Persico, Antonio
; TITLE OF INVENTION: cDNA and Genomic Clones Encoding Human
; TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-3487
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,275A
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-449P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
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; NAME/KEY: -
; LOCATION: 1..2160
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; OTHER INFORMATION: /note="cDNA encoding human mu opiate receptor"
US-08-188-275A-1

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Best Local Similarity 98.6%; Pred. No. 1.7e-13;
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Db 328 GCACCTGTGCCGACCATCGGTCCGAACCGACGACCTGTGGCGGAGAGACAGCCTGT 387

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RESULT 4
US-09-351-198-1
; Sequence 1, Application US/09351198
; Patent No. 6335168
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226N
; CURRENT APPLICATION NUMBER: US/09/351,198
; CURRENT FILING DATE: 1999-07-09

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; EARLIER APPLICATION NUMBER: 60/092,402
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
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; SEQ ID NO 1
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; LOCATION: (2063)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2091)
; OTHER INFORMATION: No. 6335168feature for this position in GeneBank.
US-09-351-198-1

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Query Match          97.7%; Score 69.4; DB 4; Length 2162;
Best Local Similarity 98.6%; Pred. No. 1.7e-13;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 61 GCCCTCCGACC 71
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RESULT 5
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; Sequence 1, Application US/09113426
; Patent No. 6337207
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary J
; APPLICANT: Laforge, Karl S
; APPLICANT: Yu, Lei
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: ALLELES OF THE HUMAN MU OPIOID RECEPTOR, DIAGNOSTIC
; TITLE OF INVENTION: METHODS OF USING SAID ALLELES, AND METHODS OF TREATMENT
; TITLE OF INVENTION: BASED THEREON
; FILE REFERENCE: 600-1-226
; CURRENT APPLICATION NUMBER: US/09/113,426
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 7
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: No. 6337207feature for this position in GeneBank.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2091)
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US-09-113-426-1

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Query Match          97.7%; Score 69.4; DB 4; Length 2162;
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Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6

US-08-889-108-1
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; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cDNA)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
US-08-889-108-1

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DB 383 GCCCTCAGACC 393

RESULT 7

US-08-889-108-3
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; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston

STATE: TX

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3

Query Match

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Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 61 GCCCTCCGACC 71

DB 383 GCCCTCAGACC 393

RESULT 8

US-08-120-601B-1
; Sequence 1, Application US/08120601B
; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-08-120-601B-1

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RESULT 9
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Sequence 3, Application US/08120601B
Patent No. 6235496
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/120.601B
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1232
US-08-120-601B-3

Query Match 79.7% Score 56.6; DB 4; Length 1618;
Best Local Similarity 87.3% Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATCGGTCCGACCGACGACCTGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 GCAACCATGTCGATCCATCGGTCTGAACCGACCGGCTTGCGGAGAACAGACGCTGT 382
OY 61 GCCCTCCGACC 71
||||| |||||
DB 383 GCCCTCAGACC 393

RESULT 10
PCT-US94-10358-1
Sequence 1, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120 601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
FILING DATE: 79-0924
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
PCT-US94-10358-1

Query Match 79.7% Score 56.6; DB 5; Length 1618;
Best Local Similarity 87.3% Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATCGGTCCGACCGACGACCTGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 GCAACCATGTCGATCCATCGGTCTGAACCGACCGGCTTGCGGAGAACAGACGCTGT 382
OY 61 GCCCTCCGACC 71
||||| |||||
DB 383 GCCCTCAGACC 393

RESULT 11

PCT-US94-10358-3
Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: IND0005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
PCT-US94-10358-3

Query Match 79.7%; Score 56.6; DB 5; Length 1618;
Best Local Similarity 87.3%; Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACGTGTCGACCGATGCGGTCCGAACCGACGACCTGGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 GCAACGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 382
QY 61 GCCCTCGAC 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 383 GCCCTCGAC 393

RESULT 12
US-08-430-286A-1
Sequence 1, Application US/08430286A
Patent No. 6225080
GENERAL INFORMATION:
APPLICANT: Uhl, George R.
APPLICANT: Epler, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-Subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York

COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,286A
FILING DATE: 28-APR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: RODINSON, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A843-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2135 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
IMMEDIATE SOURCE:
CLONE: mu receptor cDNA
US-08-430-286A-1

Query Match 79.7%; Score 56.6; DB 4; Length 2135;
Best Local Similarity 87.3%; Pred. No. 1.7e-09;
Matches 62; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCAACGTGTCGACCGATGCGGTCCGAACCGACGACCTGGGCGGAGAGACAGCCTGT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 GCAACGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 199
QY 61 GCCCTCGAC 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 GCCCTCGAC 210

RESULT 13
US-08-387-707-15
Sequence 15, Application US/08387707
Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,707
FILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959

```
REFERENCE/DOCKET NUMBER: 22000-20526.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-387-707-15

Query Match
Best Local Similarity 84.5%; Score 53.4; DB 4; Length 1981;
Matches 60; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GCAACCTGCGACCCATCGGTCCGACCGACCGACCTGGGGGAGAGACAGCCTGT 60
DB 365 GAAACGACGATCGCGATCGGTCTTAACCGACGCGGCTTGGCGGAGACAGCCTGT 424

QY 61 GCGCTCCGAC 71
DB 425 GCGCTCCGAC 435

RESULT 14
US-09-171-461-29
Sequence 29, Application US/09171461
Patent No. 6335016
GENERAL INFORMATION:
APPLICANT: Baker, Adam
APPLICANT: Cotten, Matthew
APPLICANT: Chiocca, Susanna
APPLICANT: Kurzbauner, Robert
APPLICANT: Schaffner, Gotthold
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800000
CURRENT APPLICATION NUMBER: US/09/171,461
EARLIER FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: PCT/EP97/01944
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 1728
TYPE: DNA
ORGANISM: CELO VIRUS
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1728)
US-09-171-461-29

Query Match
Best Local Similarity 34.1%; Score 24.2; DB 4; Length 1728;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 CAACCTGTCGACCCATCGGTCCGACCGACCGACCTGGGGGAGAGACAGCCTGTG 61
DB 801 CACCTCTGACGCGCGGTAAACGACCGACCGCGCTTGGCCCTTAAGAGACCGCACGG 860

QY 62 C 62
DB 861 C 861

RESULT 15
US-09-171-461-1/c
Sequence 1, Application US/09171461
Patent No. 6335016
GENERAL INFORMATION:
APPLICANT: Baker, Adam
APPLICANT: Cotten, Matthew
APPLICANT: Chiocca, Susanna
APPLICANT: Kurzbauner, Robert
APPLICANT: Schaffner, Gotthold
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800000
CURRENT APPLICATION NUMBER: US/09/171,461
EARLIER FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: PCT/EP97/01944
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 43804
TYPE: DNA
ORGANISM: CELO Virus
FEATURE:
NAME/KEY: gene
LOCATION: (12193)..(15043)
OTHER INFORMATION: /gene: L1
FEATURE:
NAME/KEY: misc.feature
LOCATION: (15080)
OTHER INFORMATION: /note= L2 region penton base splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (15110)..(17495)
OTHER INFORMATION: /gene: L2
FEATURE:
NAME/KEY: polyA_site
LOCATION: (17526)
FEATURE:
NAME/KEY: gene
LOCATION: (17559)..(21754)
OTHER INFORMATION: /gene: L3
FEATURE:
NAME/KEY: misc.feature
LOCATION: (18261)
OTHER INFORMATION: /gene: L3 /note= hexon splice acceptor site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (21102)
OTHER INFORMATION: /gene: L3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (21123)
OTHER INFORMATION: /gene: L3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21767)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21824)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21836)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21882)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (23608)
OTHER INFORMATION: /note= 100K splice acceptor site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (23649)
OTHER INFORMATION: /note= 100K splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (23680)..(27886)
OTHER INFORMATION: /gene: L4
FEATURE:
NAME/KEY: polyA_site
LOCATION: (27920)
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (28315)
OTHER INFORMATION: /note= fibre splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28341)
OTHER INFORMATION: / note= fibre splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (28363)..(31768)
OTHER INFORMATION: /gene: L5
FEATURE:
NAME/KEY: misc_feature
LOCATION: (30511)
OTHER INFORMATION: /gene: L5 /note= fibre splice acceptor site
FEATURE:
NAME/KEY: polyA_site
LOCATION: (31770)
US-09-171-461-1

Query Match 34.1%; Score 24.2; DB 4; Length 43804;
Best Local Similarity 62.3%; Pred. No. 27;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 2 CAACCTGTCGACCCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGTG 61
Db 11196 CACCTCTGAGCGCGGCGGTAAACGACCGACCGCGCTGCGCCCTAGAGACCGCACGG 11137

OY 62 C 62
Db 11136 C 11136

RESULT 16
US-08-727-688-1
Sequence 1, Application US/08727688
Patent No. 5919638
GENERAL INFORMATION:
APPLICANT: Russell, John C.
TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road D377/AP6D
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,688
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poremski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5967.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 937-0378
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-727-688-1

Query Match 33.8%; Score 24; DB 2; Length 367;
Best Local Similarity 60.9%; Pred. No. 21;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
Db 107 GAAACGAGTGGACCTAGTGGCTCTCAACCTGCTTCCCTCGGGGTGGCGTGGCGCTGA 166

OY 61 GCCC 64
Db 167 CCCC 170

RESULT 17
US-08-727-688-9
Sequence 9, Application US/08727688
Patent No. 5919638

GENERAL INFORMATION:
APPLICANT: Russell, John C.
TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road D377/AP6D
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,688

FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poremski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5967.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 937-0378
TELEFAX: (847) 938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-727-688-9

Query Match 33.8%; Score 24; DB 2; Length 1297;
Best Local Similarity 60.9%; Pred. No. 23;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 1 GCAACCTGTCGACCCATGCGGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGT 60
Db 107 GAAACGAGTGGACCTAGTGGCTCTCAACCTGCTTCCCTCGGGGTGGCGTGGCGCTGA 166

OY 61 GCCC 64
Db 167 CCCC 170

RESULT 18

US-09-020-956-109
; Sequence 109, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-109
Query Match 33.8%; Score 24; DB 4; Length 1524;
Best Local Similarity 60.9%; Pred. No. 24;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GCAACCTGCCAGCCATCGGTCCGACCGACCGACCTGGCGGAGAGACAGCCTGT 60
DB 116 GGAACGAGTGCAGCTAGTGGCTTCACCTGCTCTCCTGGCGGTGGCGCTGCCGCTGA 175
QY 61 GCCC 64
DB 176 CCCG 179
RESULT 19
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-109
Query Match 33.8%; Score 24; DB 4; Length 1524;
Best Local Similarity 60.9%; Pred. No. 24;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GCAACCTGCCAGCCATCGGTCCGACCGACCGACCTGGCGGAGAGACAGCCTGT 60
DB 116 GGAACGAGTGCAGCTAGTGGCTTCACCTGCTCTCCTGGCGGTGGCGCTGCCGCTGA 175
QY 61 GCCC 64
DB 176 CCCG 179
RESULT 20
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retler, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-109
Query Match 33.8%; Score 24; DB 4; Length 1524;
Best Local Similarity 60.9%; Pred. No. 24;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GCAACCTGCCAGCCATCGGTCCGACCGACCGACCTGGCGGAGAGACAGCCTGT 60
DB 116 GGAACGAGTGCAGCTAGTGGCTTCACCTGCTCTCCTGGCGGTGGCGCTGCCGCTGA 175


```

; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Query Match          32.7%; Score 23.2; DB 4; Length 6816;
Best Local Similarity 58.8%; Pred. No. 47;
Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGTCCGACGACGACCTGGGGGAGAGACAGCCTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6517 GCAGCCTGGCCCCCGCCCGCCCGCCCGACGCGCCGCTGGCCACAGGCTGGCCGGA 6576

QY 61 GCCCTCCG 68
    ||| ||
DB 6577 GCCCTCCG 6584

RESULT 25
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietlich, Paul S.
; APPLICANT: McIver, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS: COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3

Query Match          32.7%; Score 23.2; DB 4; Length 6855;
Best Local Similarity 58.8%; Pred. No. 47;
Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GCAACCTGTCGACCCATGCGTCCGACGACGACCTGGGGGAGAGACAGCCTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6556 GCAGCCTGGCCCCCGCCCGCCCGCCCGACGCGCCGCTGGCCACAGGCTGGCCGGA 6615

QY 61 GCCCTCCG 68
    ||| ||
DB 6616 GCCCTCCG 6623

RESULT 26
US-09-030-607-195/C
; Sequence 195, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-030-607-195
```

```

Query Match          32.4%; Score 23; DB 4; Length 502;
Best Local Similarity 58.5%; Pred. No. 44;
Matches 38; Conservative 1; Mismatches 26; Indels 0; Gaps 0;
```

```

QY 7 TGTCCGACCCATGCGTCCGACGACGACCTGGGGGAGAGACAGCCTGTGCCCTC 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 278 TGTGTGATCCAGAGACTCAGGGGCTCTTCTGTGGGGGACACAGACCCCTTCCCTT 219

QY 67 CGACC 71
    ||
DB 218 CCTCC 214
```

```

RESULT 27
US-09-439-313-195/C
; Sequence 195, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reltter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
```


NAME/KEY: CDS
LOCATION: 303..1334
US-08-590-563-1

Query Match 32.4%; Score 23; DB 4; Length 1375;
Best Local Similarity 57.7%; Pred. No. 48;
Matches 41; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 GGAACCTGTCGACCCATCGGTCCGAACCGACCGACTGGCGGAGAGACAGCTGT 60
DB 886 GGAACCACTTGGAGCGCTGGCGCGCGGCATGACCTGGCAGACCACTTACCAGA 945
QY 61 GCCCTCCGACC 71
DB 946 TCATGCCGACC 956

RESULT 30
PCT-US91-06532-1
Sequence 1, Application PC/TUS9106532
GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza Suite 2100
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06532
FILING DATE: 19910910
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27373/8235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEFAX: 312/984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US91-06532-1

Query Match 32.1%; Score 22.8; DB 5; Length 1335;
Best Local Similarity 59.1%; Pred. No. 55;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 6 CTGTCCGACCCATCGGTCCGAACCGACCGACTGGCGGAGAGACAGCTGTGCTCT 65
DB 428 CCGCCCCCGCGCGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAACCCCT 487
QY 66 CGGACC 71
DB 488 CCCACC 493

RESULT 31

US-08-247-901C-1/c
Sequence 1, Application US/08247901C
Patent No. 5750384
GENERAL INFORMATION:
APPLICANT: Jacobs et al
TITLE OF INVENTION: L5 SHUTTLE PHASMIDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Ebenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,901C
FILING DATE: May 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/057,531
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/273
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-381-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 50341
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: L5 shuttle phasmid sequence
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: L5 mycobacteriophage
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION: No. 5750384e
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-247-901C-1

Query Match 32.1%; Score 22.8; DB 1; Length 50341;
Best Local Similarity 59.1%; Pred. No. 73;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCCATGCGTCCGACCGACCGCTGGCGGAGAGACAGCTGTGCC 64
Db 31163 CCAGCGCTACTGGCGGTATGAGCAGAAAGATCTCGCCGAGAACTACGCGTGAACCC 31104

QY 65 TCCGAC 70
Db 31103 TGCCAC 31098

RESULT 32
US-09-075-904-1/C
Sequence 1, Application US/09075904
Patent No. 5994137
GENERAL INFORMATION:
APPLICANT: Jacobs, et al.
TITLE OF INVENTION: L5 SHUTTLE PHASMIDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Epenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,904
FILING DATE: May 11, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,901
FILING DATE: May 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/475
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 50341
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: L5 shuttle plasmid sequence
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: L5 mycobacteriophage
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:

POSITION IN GENOME:
CHROMOSOME/SEGMENT:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION: No. 5994137e
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-075-904-1

Query Match 32.1%; Score 22.8; DB 2; Length 50341;
Best Local Similarity 59.1%; Pred. No. 73;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCCATGCGTCCGACCGACCGCTGGCGGAGAGACAGCTGTGCC 64
Db 31163 CCAGCGCTACTGGCGGTATGAGCAGAAAGATCTCGCCGAGAACTACGCGTGAACCC 31104

QY 65 TCCGAC 70
Db 31103 TGCCAC 31098

RESULT 33
US-09-426-436-1/C
Sequence 1, Application US/09426436
Patent No. 622506
GENERAL INFORMATION:
APPLICANT: William R. Jacobs, Jr.
APPLICANT: Barry R. Bloom
APPLICANT: Graham F. Halfull
TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC
TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Epenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/426,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/705,557
FILING DATE:
APPLICATION NUMBER: US/08/057,531
FILING DATE:
APPLICATION NUMBER: 07/833,431
FILING DATE: February 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: 96700/238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52297
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: phage genome sequence
HYPOTHETICAL: no
ANTISENSE: no
FRAGMENT TYPE: not applicable.
ORIGINAL SOURCE:
ORGANISM: mycobacteriophage L5
STRAIN: not applicable
INDIVIDUAL ISOLATE: L5
DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: not applicable
CELL TYPE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Hatfull and Sarkis
TITLE: DNA Sequence, Structure and Gene
TITLE: Expression of Mycobacteriophage L5:
TITLE: A Phage System for Mycobacterial
TITLE: Genetics
JOURNAL: Molecular Microbiology
VOLUME: 7
PAGES: 395-405
DATE: 1993
US-09-426-436-1

Query Match 32.1%; Score 22.8; DB 4; Length 52297;
Best Local Similarity 59.1%; Pred. No. 73;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCATGCGGTCCGACCGACGACCTGGGGGAGAGACAGCCTGTGCC 64
DB 31060 CCAGCGCTACTGGCGGTATGATGACGAGAGATCTCGCCGAGAACTACGGCGTGAACCC 31001

QY 65 TCCGAC 70
DB 31000 TCCGAC 30995

RESULT 34
US-08-705-557-1/C
Sequence 1, Application US/08705557
Patent No. 6300061
GENERAL INFORMATION:
APPLICANT: William R. Jacobs, Jr.
APPLICANT: Barry R. Bloom
APPLICANT: Graham F. Hatfull
TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC
TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Ebenstein
STREET: 90 Park Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,557
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/057,531
FILING DATE:
APPLICATION NUMBER: 07/833,431
FILING DATE: February 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pasquallini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: 96700/238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52297
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: phage genome sequence
HYPOTHETICAL: no
ANTISENSE: no
FRAGMENT TYPE: not applicable.
ORIGINAL SOURCE:
ORGANISM: mycobacteriophage L5
STRAIN: not applicable
INDIVIDUAL ISOLATE: L5
DEVELOPMENTAL STAGE: not applicable
HAPLOTYPE: not applicable
TISSUE TYPE: not applicable
CELL TYPE: not applicable
ORGANELLE: not applicable
IMMEDIATE SOURCE: mycobacteriophage L5 particles
POSITION IN GENOME: entire genome
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Hatfull and Sarkis
TITLE: DNA Sequence, Structure and Gene
TITLE: Expression of Mycobacteriophage L5:
TITLE: A Phage System for Mycobacterial
TITLE: Genetics
JOURNAL: Molecular Microbiology
VOLUME: 7
PAGES: 395-405
DATE: 1993
US-08-705-557-1

Query Match 32.1%; Score 22.8; DB 4; Length 52297;
Best Local Similarity 59.1%; Pred. No. 73;
Matches 39; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCTGTCCGACCATGCGGTCCGACCGACGACCTGGGGGAGAGACAGCCTGTGCC 64
DB 31060 CCAGCGCTACTGGCGGTATGATGACGAGAGATCTCGCCGAGAACTACGGCGTGAACCC 31001

QY 65 TCCGAC 70
DB 31000 TCCGAC 30995

APPLICANT: Strachy, Nancy
 APPLICANT: Fantini, Susan E.
 TITLE OF INVENTION: Cloning of the biosynthetic pathway for
 TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmid
 TITLE OF INVENTION: useful therein
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,933
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,468
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

```

Query Matchc          31.8%; Score 22.6; DB 2; Length 30001;
Best Local Similarity 60.7%; Pred. No. 82;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps

OY      2  CACACTGTCGACCCATGCGGCTCCAGACCGACGACTGGCGGGAGAGACACTGTG 61
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      15440 CGAGCGCTCCGCGGGGCTCGACAGATCCGCCGCAACTCGGCGCTCCGGCACCGGCTGT 15499

OY      62 C 62
          |
Db      15500 C 15500

RESULT 43
US-08-923-137-2/C
; Sequence 2, Application US/08923137
; Patent No. 6083716
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Farina, Steven F.
; APPLICANT: Fisher, Krishna J.
; TITLE OF INVENTION: Chimpanzee Adenovirus Vectors
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: United States of America
; ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,137
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.021CIP1USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-923-137-2

```

Query Match	31.8%	Score 22.6:	DB 3	Length 36519:
Best Local Similarity	60.7%	Pred. No. 82:		
Matches	37:	Conservative	0:	Mismatches 24: Indels 0: Gaps 0:
OY	2	CAACCTGCCACCCATCGCGGCGCAACCGCCAGCAGCTGGCGGGGAGAGACAGCCTG	61	
Db	34024	CAACCTGGTGTCTGTGTGTGTCAGCAGTACTGCAGCGACGACCTGAGCCGAGATCCGATGCGCTG	33965	
OY				
	62	C	62	
Db	33964	C	33964	

```

RESULT 44
US-09-105-537-5
: Sequence 5, Application US/09105537A
: Patent No. 6265202
: GENERAL INFORMATION:
: APPLICANT: Sherman, D.H.
: APPLICANT: Liu, H.
: APPLICANT: Xue, Y.
: APPLICANT: Zhao, L.
: TITLE OF INVENTION: DNA encoding methymycin and pikromycin
: FILE REFERENCE: 600.438051
: CURRENT APPLICATION NUMBER: US/09/105,537A
: CURRENT FILING DATE: 1998-06-26
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: fastseq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 36778
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
: US-09-105-537-5

```

	Query Match	31.8%	Score 22.6;	DB 4,	Length 36778;	
	Best Local Similarity	60.7%;	Pred. No. 82;			
	Matches	37;	Conservative	0;	Mismatches	24; Indels
					Gaps	0.
OY	1 GCAACCTGTCGCACCATTGCGGTCCGAACCGCAGCCACTGGCGGGAGACAGACGCTGT	60				
Db	2124 GGAAAGCCCGGACTTCTAGCACGCCGGAACGCTCGCCCCGCGCCTCGAACAAGCCGCT	2183				
OY	61 G 61					
Db	2184 G 2184					

```
RESULT 45
US-09-320-878-19
; Sequence 19, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; EARLIER FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 19
; LENGTH: 38506
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-19

Query Match          31.8%; Score 22.6; DB 3; Length 38506;
Best Local Similarity 60.7%; Pred. No. 83;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY      1  GCAACCTGTCGACCCATGGTCCGACCGCGACCGCGGCGGAGAGACAGCCTGT 60
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      266  GGAACCGCGCGCCTTCTACGACCGCGACCGCTCCGCCCGCTCGACAGCGCGGT 325

OY      61  G 61
          |  |
Db      326  G 326

RESULT 46
US-09-428-517-1/C
; Sequence 1, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Betlach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: MCDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLFANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 50937
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1
```

```
Query Match          31.8%; Score 22.6; DB 4; Length 50937;
Best Local Similarity 60.7%; Pred. No. 84;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY      10  CCGACCCATGGGTCCGACCGACCGACCTGGCGGAGAGACACCTGTGCTCCGA 69
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      43639  CCGAGAGATGAGTCCGACCCCGACAGACCGCGGTGGCGCTGCCGCGCGCGC 43580

OY      70  C 70
          |  |
Db      43579  C 43579

RESULT 47
US-09-170-331-3
; Sequence 3, Application US/09170331C
; Patent No. 6028175
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R
; APPLICANT: Grandy, David K
; TITLE OF INVENTION: A No. 6028175e1 Mammalian Methadone-Specific Opioid Receptor
; FILE REFERENCE: 93-311-C
; CURRENT APPLICATION NUMBER: US/09/170,331C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (182)..(1282)
US-09-170-331-3

Query Match          31.5%; Score 22.4; DB 3; Length 1452;
Best Local Similarity 59.4%; Pred. No. 74;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY      1  GCAACCTGTCGACCCATGGTCCGACCGCGACCGACCTGGCGGAGAGACAGCCTGT 60
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Db      240  GGAACCTGTCCTCTAATGAGACCGTACCCACCCACCTGTCTCAATGTATGATCA 299

OY      61  GCCC 64
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Db      300  GCGC 303

RESULT 48
US-08-967-101-96/C
; Sequence 96, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESLA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:32:12 : Search time 1712 Seconds

(without alignments)
559.745 Million cell updates/sec

Title: US-09-626-616-7_COPY_354_424

Perfect score: 71

Sequence: 1 GCACCGTCGCCGACCATGC.....ACACCGTCGCCGACCATGC 71

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27433522

Minimum DB seq length: 35

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :
1: em_estba:*
2: em_esthum:*
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13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 258	24	33.8	202	9	AA327303	AA327303 ESTR0615	C 331	23.8	33.5	1083	10	BF526881	BF526881 602070446
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C 261	24	33.8	296	10	T29281	T29281 EST74974 Hu	C 334	23.8	33.5	1430	10	BG855959	BG855959 1024044C0
262	24	33.8	321	9	Al916166	Al916166 w147f02.x	C 335	23.8	33.5	3141	11	BC013227	BC013227 Mms muscu
263	24	33.8	337	10	BG252938	BG252938 602365539	C 336	23.6	33.2	139	9	AM416334	AM416334 51573 MAR
C 264	24	33.8	343	9	AA792745	AA792745 v88d11.r	C 337	23.6	33.2	139	9	AM416335	AM416335 51574 MAR
C 265	24	33.8	363	10	C02794	C02794 C02794 Huma	C 338	23.6	33.2	162	12	A2342926	A2342926 1M0076111
C 266	24	33.8	364	9	AA336217	AA336217 EST40761	C 339	23.6	33.2	171	9	AM839909	AM839909 MR4-LT007
267	24	33.8	385	10	W42402	W42402 mc76e05.r1	C 340	23.6	33.2	225	10	R25625	R25625 yH45902.r1
C 268	24	33.8	387	10	BE137064	BE137064 uc959c09.x	C 341	23.6	33.2	232	10	BB495146	BB495146 BB495146
269	24	33.8	390	9	AL588333	AL588333 tq66h02.x	C 342	23.6	33.2	241	10	AA225661	AA225661 nc08c11.r
270	24	33.8	410	10	HI8835	HI8835 ym45d10.r1	C 343	23.6	33.2	243	10	Bi402715	Bi402715 M1-P-CPI-
271	24	33.8	413	12	AO973857	AO973857 RPCI-23-3	C 344	23.6	33.2	243	10	R21492	R21492 yG06e09.r1
C 272	24	33.8	418	10	BM482353	BM482353 535214 MA	C 345	23.6	33.2	252	9	AV017865	AV017865 AV017865
C 273	24	33.8	442	10	N34668	N34668 y15607.s1	C 346	23.6	33.2	292	9	BB173632	BB173632 BB173632
C 274	24	33.8	444	9	AA816479	AA816479 OVO-ST023	C 347	23.6	33.2	315	9	BB255729	BB255729 BB255729
C 275	24	33.8	452	9	AA463023	AA463023 v985b01.r	C 348	23.6	33.2	344	10	Bi184098	Bi184098 UNL-P-FN-
276	24	33.8	452	12	AO936675	AO936675 JNB-023R	C 349	23.6	33.2	344	10	Bi184719	Bi184719 UNL-P-FN-
277	24	33.8	471	10	Bi808191	Bi808191 C004D04 O	C 350	23.6	33.2	355	10	T70189	T70189 yC18c11.s1
C 278	24	33.8	475	10	BM253153	BM253153 512525 MA	C 351	23.6	33.2	371	10	BM376850	BM376850 EBem05_SQ
279	24	33.8	477	9	Al754179	Al754179 cr21d06.x	C 352	23.6	33.2	390	9	AA280987	AA280987 A43A-ABA-
280	24	33.8	480	12	BH611251	BH611251 SALR.0305	C 353	23.6	33.2	392	9	AA394294	AA394294 t269d05.r
281	24	33.8	544	9	BB754536	BB754536 BB754536	C 354	23.6	33.2	393	10	W39779	W39779 zC80H04.r1
282	24	33.8	544	9	Al427258	Al427258 mc76e05.y	C 355	23.6	33.2	400	10	BE605229	BE605229 WHE1701-1
C 283	24	33.8	574	10	BG474234	BG474234 602516854	C 356	23.6	33.2	413	9	AJ281717	AJ281717 A43A-AAR-
C 284	24	33.8	586	10	BG928724	BG928724 HNC72-1-C	C 357	23.6	33.2	425	10	BF706203	BF706203 280575 MA
285	24	33.8	609	9	Al911818	Al911818 wC86903.x	C 358	23.6	33.2	443	10	BF327484	BF327484 OVA-BN009
C 286	24	33.8	610	12	AG130993	AG130993 Pan trogl	C 359	23.6	33.2	445	9	AA313759	AA313759 EST183407
287	24	33.8	620	9	AM851731	AM851731 MR2-CT022	C 360	23.6	33.2	449	10	BF514268	BF514268 UT-H-BM1-
288	24	33.8	672	10	Bi759746	Bi759746 603045620	C 361	23.6	33.2	453	9	BB773282	BB773282 BB773282
289	24	33.8	694	10	BE372473	BE372473 601223918	C 362	23.6	33.2	462	10	BF189037	BF189037 234294 MA
290	24	33.8	699	12	AG114683	AG114683 Pan trogl	C 363	23.6	33.2	464	9	AJ282617	AJ282617 A43A-ABA-
291	24	33.8	745	9	Al996994	Al996994 701551562	C 364	23.6	33.2	470	10	BF405458	BF405458 UT-R-CA1-
292	24	33.8	746	10	BE883638	BE883638 601507317	C 365	23.6	33.2	479	10	C03257	C03257 C03257 Huma
293	24	33.8	845	9	AL533517	AL533517 AL533517	C 366	23.6	33.2	488	12	CNS01SAB	AL164972 Tetraodon
294	24	33.8	847	9	AL576856	AL576856 AL576856	C 367	23.6	33.2	497	10	BF118093	BF118093 uc11907.y
C 295	24	33.8	891	10	BF131004	BF131004 601820049	C 368	23.6	33.2	499	12	AQ397939	AQ397939 m9xb0007C
296	24	33.8	900	10	BF981740	BF981740 602306096	C 369	23.6	33.2	500	9	AV393411	AV393411 AV393411
297	24	33.8	975	10	BF302143	BF302143 602033093	C 370	23.6	33.2	525	12	CNS03NEM	AL195195 Tetraodon
298	24	33.8	1463	10	BM472176	BM472176 AGENCOURT	C 371	23.6	33.2	530	10	BF360375	BF360375 387255 MA
299	23.8	33.5	256	10	BF336269	BF336269 RCI-CT050	C 372	23.6	33.2	530	10	BF394554	BF394554 UT-R-CA0-
300	23.8	33.5	361	12	AO635033	AO635033 RCI-11-4	C 373	23.6	33.2	545	10	BE645586	BE645586 7672f05.x
301	23.8	33.5	407	9	AV760910	AV760910 AV760910	C 374	23.6	33.2	577	9	AM851713	AM851713 MR2-CT022
C 302	23.8	33.5	431	9	AV429944	AV429944 AV429944	C 375	23.6	33.2	587	10	BF334111	BF334111 MR2-CT022
C 303	23.8	33.5	443	9	Al366203	Al366203 a087f09.x	C 376	23.6	33.2	606	12	A2378787	A2378787 1M0133009
C 304	23.8	33.5	455	12	AO865840	AO865840 nbe00026M	C 377	23.6	33.2	609	12	A2104313	A2104313 RPCI-23-4
C 305	23.8	33.5	507	9	AV431515	AV431515 AV431515	C 378	23.6	33.2	613	9	AM180918	AM180918 M9A0036T
C 306	23.8	33.5	513	9	AV431804	AV431804 AV431804	C 379	23.6	33.2	613	9	AM745961	AM745961 W61-38-AL
C 307	23.8	33.5	520	9	AV434158	AV434158 AV434158	C 380	23.6	33.2	614	9	AV721387	AV721387 AV721387
C 308	23.8	33.5	532	9	AV434812	AV434812 AV434812	C 381	23.6	33.2	618	12	CNS02J82	AL199883 Tetraodon
C 309	23.8	33.5	590	12	CNS02JTC4	AL121989 Tetraodon	C 382	23.6	33.2	626	9	AM851676	AM851676 MR2-CT022

C 383	23.6	33.2	632	9	AW949652	AW949652 EST361722	456	23.4	33.0	377	9	AA652181	AA652181 ns57e02.s
C 384	23.6	33.2	636	10	BI400787	BI400787 MI-P-AVI-	C 457	23.4	33.0	377	9	AA577960	AA577960 n12aC07.s
C 385	23.6	33.2	638	12	AZ396468	AZ396468 IM0161101	C 458	23.4	33.0	377	10	BI042734	BI042734 CM4-OT016
C 386	23.6	33.2	642	9	BB549917	BB549917 BB549917	C 459	23.4	33.0	378	10	BE938422	BE938422 RCO-TN007
C 387	23.6	33.2	650	10	BM015362	BM015362 603641525	C 460	23.4	33.0	380	9	AI161323	AI161323 qb66607.x
C 388	23.6	33.2	653	10	BI157799	BI157799 602823127	C 461	23.4	33.0	383	9	AI888548	AI888548 wn21904.x
C 389	23.6	33.2	656	9	BB539838	BB539838 BB539838	C 462	23.4	33.0	385	9	AI810886	AI810886 lu21c12.x
C 390	23.6	33.2	663	10	BI662543	BI662543 603305351	C 463	23.4	33.0	386	9	AA335066	AA335066 EST39445
C 391	23.6	33.2	672	10	BI661031	BI661031 603304339	C 464	23.4	33.0	386	10	BE938445	BE938445 RCO-TN007
C 392	23.6	33.2	677	10	BI185172	BI185172 UNL-P-FN-	C 465	23.4	33.0	389	9	AA534063	AA534063 n197c04.s
C 393	23.6	33.2	683	12	AC132858	AC132858 Pan trogl	C 466	23.4	33.0	390	9	AI810599	AI810599 tu01902.x
C 394	23.6	33.2	689	12	AQ482454	AQ482454 RPCI-11*2	C 467	23.4	33.0	390	10	C97720	C97720 C97720 Rice
C 395	23.6	33.2	705	10	BI654925	BI654925 603282879	C 468	23.4	33.0	393	9	AA600813	AA600813 MK3-OM006
C 396	23.6	33.2	726	12	BF404641	BF404641 nbXD0049M	C 469	23.4	33.0	393	9	AA593138	AA593138 ng02f06.s
C 397	23.6	33.2	737	10	BI288815	BI288815 603074960	C 470	23.4	33.0	393	10	BE722750	BE722750 191111 MA
C 398	23.6	33.2	775	10	CNS01MFU	AI170355 Tetradodon	C 471	23.4	33.0	396	9	AI188192	AI188192 qd66203.x
C 399	23.6	33.2	790	12	BI1833274	BI1833274 UNL-P-FN-	C 472	23.4	33.0	396	9	AI866906	AI866906 ml2603.x
C 400	23.6	33.2	793	10	BI1833274	BI1833274 UNL-P-FN-	C 473	23.4	33.0	397	9	AA411471	AA411471 zv22d01.s
C 401	23.6	33.2	820	12	AZ126265	AZ126265 OSJNB007	C 474	23.4	33.0	397	9	AA599342	AA599342 q935112.s
C 402	23.6	33.2	838	10	BF104750	BF104750 601822423	C 475	23.4	33.0	397	9	AA628085	AA628085 ns67d07.s
C 403	23.6	33.2	879	10	BI837697	BI837697 603086554	C 476	23.4	33.0	400	9	AI201551	AI201551 q974912.x
C 404	23.6	33.2	896	10	BI183684	BI183684 UNL-P-FN-	C 477	23.4	33.0	405	9	AA401287	AA401287 z63607.r
C 405	23.6	33.2	916	10	BI558770	BI558770 603241491	C 478	23.4	33.0	410	9	AI289756	AI289756 qv91f06.x
C 406	23.6	33.2	916	10	BI558077	BI558077 HVSMB001	C 479	23.4	33.0	415	9	AA703567	AA703567 z14c11.s
C 407	23.6	33.2	927	9	AL527283	AL527283 AL527283	C 480	23.4	33.0	415	9	AI125356	AI125356 q92d09.x
C 408	23.6	33.2	937	10	BI588226	BI588226 HVSMB001	C 481	23.4	33.0	415	9	N21064	N21064 y447g10.s1
C 409	23.6	33.2	942	10	BF539195	BF539195 602053059	C 482	23.4	33.0	421	10	BM027803	BM027803 020 Inter
C 410	23.6	33.2	1391	12	AC079973	AC079973 Pan trogl	C 483	23.4	33.0	425	10	BE938518	BE938518 RCO-TN007
C 411	23.6	33.2	1398	10	BC025584	BC025584 602274503	C 484	23.4	33.0	427	9	AI880411	AI880411 at55c09.x
C 412	23.6	33.2	1512	10	BI489196	BI489196 603021413	C 485	23.4	33.0	427	9	AA259219	AA259219 nc17f05.r
C 413	23.6	33.2	1568	12	AC076526	AC076526 Pan trogl	C 486	23.4	33.0	430	12	AA032275	AA032275 HS_2194_B
C 414	23.6	33.2	1620	10	BE903393	BE903393 601675925	C 487	23.4	33.0	436	9	AI280652	AI280652 qu04008.x
C 415	23.6	33.2	1664	10	BE962090	BE962090 601655162	C 488	23.4	33.0	438	10	BE808295	BE808295 213463 MA
C 416	23.4	33.0	117	9	AW865189	AW865189 PM3-SN002	C 489	23.4	33.0	439	10	R50336	R50336 y159603.s1
C 417	23.4	33.0	126	9	AA458880	AA458880 zx88b07.s	C 490	23.4	33.0	440	9	AI301508	AI301508 qn44910.x
C 418	23.4	33.0	187	9	AA588880	AA588880 zx88b07.s	C 491	23.4	33.0	440	10	BE771975	BE771975 CM3-F7010
C 419	23.4	33.0	228	10	BF092131	BF092131 RCO-TN007	C 492	23.4	33.0	446	9	AI076047	AI076047 oy06c12.x
C 420	23.4	33.0	241	9	AW428130	AW428130 64991 MAR	C 493	23.4	33.0	448	10	BE926320	BE926320 HNC51-I-B
C 421	23.4	33.0	243	9	AA659908	AA659908 nv03d02.s	C 494	23.4	33.0	450	10	N80216	N80216 z019e04.s1
C 422	23.4	33.0	259	9	AA365426	AA365426 EST76376	C 495	23.4	33.0	450	12	AQ592474	AQ592474 HS_5455_A
C 423	23.4	33.0	260	9	AA541749	AA541749 n187d11.s	C 496	23.4	33.0	452	9	AI832585	AI832585 at7004.x
C 424	23.4	33.0	266	9	AA316985	AA316985 EST18930	C 497	23.4	33.0	454	9	AI086832	AI086832 c257h02.x
C 425	23.4	33.0	273	9	AI817603	AI817603 wK39d06.x	C 498	23.4	33.0	454	12	AQ0937398	AQ0937398 NB2-007R
C 426	23.4	33.0	276	9	AW797008	AW797008 QV1-UM003	C 499	23.4	33.0	455	9	AI304521	AI304521 q054n03.x
C 427	23.4	33.0	281	9	AI685742	AI685742 t437f02.x	C 500	23.4	33.0	455	9	AI797199	AI797199 w63b11.s
C 428	23.4	33.0	281	9	AW016211	AW016211 UT-H-B10P	C 501	23.4	33.0	455	9	AA455032	AA455032 zx96f08.s
C 429	23.4	33.0	287	10	BF386067	BF386067 UI-R-CA0-	C 502	23.4	33.0	457	9	AI282395	AI282395 qu93e01.x
C 430	23.4	33.0	289	9	AA578385	AA578385 n131c08.s	C 503	23.4	33.0	460	9	AI087181	AI087181 g259h06.x
C 431	23.4	33.0	291	9	AA348877	AA348877 EST55455	C 504	23.4	33.0	460	9	AA401077	AA401077 zu51f02.s
C 432	23.4	33.0	292	9	AI811810	AI811810 tW32d08.x	C 505	23.4	33.0	463	9	AI266127	AI266127 qp64d07.x
C 433	23.4	33.0	294	9	AW068126	AW068126 cN23e01.x	C 506	23.4	33.0	464	10	R51320	R51320 y972f05.s1
C 434	23.4	33.0	295	9	AA781200	AA781200 a124g04.s	C 507	23.4	33.0	466	9	AI371879	AI371879 ta06b04.x
C 435	23.4	33.0	303	9	AA853433	AA853433 NHTBCae05	C 508	23.4	33.0	466	10	BF055306	BF055306 qf98b07.x
C 436	23.4	33.0	303	9	AI826654	AI826654 wK35g08.x	C 509	23.4	33.0	467	9	AI200366	AI200366 qf98b07.x
C 437	23.4	33.0	306	9	AA670072	AA670072 q937h06.s	C 510	23.4	33.0	468	9	AI749608	AI749608 at25b09.x
C 438	23.4	33.0	306	9	AA877166	AA877166 o1v7g06.s	C 511	23.4	33.0	471	12	AQ201171	AQ201171 RPCI11-46
C 439	23.4	33.0	309	9	AI886703	AI886703 wh18f09.x	C 512	23.4	33.0	472	9	AI080529	AI080529 qz63e04.x
C 440	23.4	33.0	314	9	AA503968	AA503968 nh39a09.s	C 513	23.4	33.0	473	9	BB839928	BB839928 BB839928
C 441	23.4	33.0	317	9	AA662264	AA662264 nu93b07.s	C 514	23.4	33.0	474	10	N29929	N29929 yw53a08.s1
C 442	23.4	33.0	317	9	AA232779	AA232779 zt48g07.r	C 515	23.4	33.0	474	10	BE843841	BE843841 RCO-TN007
C 443	23.4	33.0	322	9	AA578194	AA578194 n129h02.s	C 516	23.4	33.0	481	9	AA534237	AA534237 n170e07.s
C 444	23.4	33.0	322	9	AA578224	AA578224 n122a01.s	C 517	23.4	33.0	485	9	AI189885	AI189885 qd29b10.x
C 445	23.4	33.0	327	10	BF092984	BF092984 MR4-TN011	C 518	23.4	33.0	489	9	AA447630	AA447630 zw97c06.s
C 446	23.4	33.0	328	9	AA285101	AA285101 zt23c03.r	C 519	23.4	33.0	490	9	AA834008	AA834008 of25a10.s
C 447	23.4	33.0	331	9	AI798639	AI798639 wG35g10.x	C 520	23.4	33.0	491	9	AI284586	AI284586 ml06c04.x
C 448	23.4	33.0	344	10	F21073	F21073 HSPD05541 H	C 521	23.4	33.0	492	9	AA552327	AA552327 nk06h12.s
C 449	23.4	33.0	348	9	AI273009	AI273009 qv63f07.x	C 522	23.4	33.0	497	9	AA600270	AA600270 af01e11.s
C 450	23.4	33.0	352	9	AA427777	AA427777 zw33g10.s	C 523	23.4	33.0	502	9	AA595356	AA595356 no36c01.s
C 451	23.4	33.0	352	9	AA515428	AA515428 nt69c08.s	C 524	23.4	33.0	505	9	AA595165	AA595165 ou54c12.s
C 452	23.4	33.0	360	9	AA533702	AA533702 n192a11.s	C 525	23.4	33.0	506	9	AA743928	AA743928 bs05d12.s
C 453	23.4	33.0	363	9	AI239427	AI239427 qh31b05.x	C 526	23.4	33.0	508	9	AI749142	AI749142 at29g06.x
C 454	23.4	33.0	370	9	AI866979	AI866979 wh14d02.x	C 527	23.4	33.0	512	10	BE910359	BE910359 60280573
C 455	23.4	33.0	373	10	BF115460	BF115460 7n83c07.x	C 528	23.4	33.0	513	9	AW339871	AW339871 ha61a01.x

529	23.4	33.0	514	9	A1288407	qV89b04.x	C 602	23.4	33.0	908	10	BF315427	BF315427	601899240
530	23.4	33.0	515	9	AA564063	nJ03c02.s	C 603	23.4	33.0	924	10	BF966418	BF966418	602287016
531	23.4	33.0	515	10	BE501657	h162b01.x	C 604	23.4	33.0	1004	10	BF188417	BF188417	603020915
532	23.4	33.0	516	9	AA437391	zw25h08.s	C 605	23.4	33.0	1093	10	B1490590	B1490590	603032243
533	23.4	33.0	517	9	AA496371	zv37e09.s	C 606	23.4	33.0	1104	10	BG117157	BG117157	602346434
C 534	23.4	33.0	517	9	AA533527	nJ96d08.s	C 607	23.4	33.0	1186	10	B117106	B117106	602868209
535	23.4	33.0	518	9	AA427585	zw33b01.s	C 608	23.4	33.0	1410	10	BG714387	BG714387	602669707
536	23.4	33.0	518	9	AA525853	n193b12.s	C 609	23.4	33.0	1788	10	BF572288	BF572288	602077734
537	23.4	33.0	518	10	W81224	z4d85e08.s1	C 610	23.2	32.7	188	10	BE46846	BE46846	175166.BA
538	23.4	33.0	518	10	BE628128	HVSMED000	C 611	23.2	32.7	241	10	B1610768	B1610768	RH16534.s
539	23.4	33.0	521	9	A1521390	L105h04.x	C 612	23.2	32.7	246	10	BG690435	BG690435	338979.BA
540	23.4	33.0	523	9	A1367324	qV95a01.x	C 613	23.2	32.7	251	10	F10372	F10372	HSC3EB102.n
541	23.4	33.0	524	9	A1635503	ts65h12.x	C 614	23.2	32.7	262	9	BB595268	BB595268	BB595268
542	23.4	33.0	528	9	AA932637	oo58b04.s	C 615	23.2	32.7	267	10	B1976368	B1976368	485227.MA
543	23.4	33.0	529	9	AA954972	op24c10.s	C 616	23.2	32.7	296	9	A1200966	A1200966	qf68g02.x
544	23.4	33.0	535	9	A1191324	qe48d05.x	C 617	23.2	32.7	296	9	BB108942	BB108942	BB108942
545	23.4	33.0	538	9	AL048329	DKExPS6B	C 618	23.2	32.7	340	9	AL512006	AL512006	267430.MA
546	23.4	33.0	539	9	AA936956	oo65e10.s	C 619	23.2	32.7	351	10	BF602245	BF602245	BF602245
C 547	23.4	33.0	540	9	A1222841	qp39g07.x	C 620	23.2	32.7	352	10	BF822879	BF822879	MRI-RT007
C 548	23.4	33.0	548	10	BE395678	601309670	C 621	23.2	32.7	352	10	BF823196	BF823196	MRI-RT007
C 549	23.4	33.0	550	10	BE391165	601286734	C 622	23.2	32.7	362	10	BF983191	BF983191	602308213
550	23.4	33.0	552	9	AA598926	ag24f04.s	C 623	23.2	32.7	377	9	AJ280791	AJ280791	4A3A-AAT-
551	23.4	33.0	554	9	A1459873	ar83c10.x	C 624	23.2	32.7	394	9	AA395502	AA395502	27285.Lam
552	23.4	33.0	555	9	A1707459	as90e07.x	C 625	23.2	32.7	397	10	BM375425	BM375425	EBEm06_SQ
553	23.4	33.0	557	9	A1672913	we74a08.x	C 626	23.2	32.7	401	9	AL449633	AL449633	AL449633
554	23.4	33.0	558	9	A1769112	wg32h06.x	C 627	23.2	32.7	445	10	BM368328	BM368328	EBed01.SQ
555	23.4	33.0	559	9	AM068546	cn21a11.x	C 628	23.2	32.7	464	10	BB796203	BB796203	BB796203
556	23.4	33.0	560	10	BM190310	POSM01000	C 629	23.2	32.7	464	10	H78033	H78033	yu85d12.r1
557	23.4	33.0	563	9	A1267900	qo22h09.x	C 630	23.2	32.7	467	10	BG691772	BG691772	341098.BA
558	23.4	33.0	563	9	AA541667	n188f04.s	C 631	23.2	32.7	466	10	BM029732	BM029732	488070.MA
559	23.4	33.0	567	9	AA518701	xs89e12.x	C 632	23.2	32.7	474	9	AL500762	AL500762	AL500762
560	23.4	33.0	568	9	A1188975	qdz2c09.x	C 633	23.2	32.7	474	9	AL504028	AL504028	AL504028
561	23.4	33.0	568	9	AM008141	vw50e11.x	C 634	23.2	32.7	475	9	AL505305	AL505305	AL505305
562	23.4	33.0	569	9	AA541745	ni87b04.s	C 635	23.2	32.7	475	10	BE412626	BE412626	MC6001.G0
563	23.4	33.0	571	9	AA706831	zj30f06.s	C 636	23.2	32.7	477	9	AL502577	AL502577	AL502577
564	23.4	33.0	572	9	AA594873	no21e08.s	C 637	23.2	32.7	490	12	AQ149125	AQ149125	HS_3165_A
565	23.4	33.0	573	9	AA541782	n187g09.s	C 638	23.2	32.7	493	9	AV911975	AV911975	AV911975
566	23.4	33.0	574	9	AA595194	no32f08.s	C 639	23.2	32.7	494	9	AW369399	AW369399	OVI-BN000
C 567	23.4	33.0	578	10	BM073281	BM073281	C 640	23.2	32.7	498	10	BM430021	BM430021	10no28EB
568	23.4	33.0	585	9	A1185277	qe31d10.s	C 641	23.2	32.7	500	12	AQ374839	AQ374839	RCIT11-14
569	23.4	33.0	590	9	AA595291	no35c01.s	C 642	23.2	32.7	510	10	BG246054	BG246054	602358887
570	23.4	33.0	595	9	A1749865	at33d12.x	C 643	23.2	32.7	513	12	AQ149120	AQ149120	HS_3165_A
571	23.4	33.0	596	9	AA514815	xu88f04.x	C 644	23.2	32.7	515	12	AV909875	AV909875	AV909875
572	23.4	33.0	601	9	AL515013	AL515013	C 645	23.2	32.7	515	12	AQ149124	AQ149124	HS_3165_A
573	23.4	33.0	602	9	A1457407	l173d07.x	C 646	23.2	32.7	518	12	AZ601376	AZ601376	1M0419K01
C 574	23.4	33.0	602	9	AA600983	nJ28c03.s	C 647	23.2	32.7	533	9	BE129089	BE129089	894020B03
C 575	23.4	33.0	634	10	BM080795	MEST113-E	C 648	23.2	32.7	540	10	BM254132	BM254132	515480.MA
576	23.4	33.0	635	9	AA905294	oJ96c09.s	C 649	23.2	32.7	541	10	BM087329	BM087329	500073.MA
577	23.4	33.0	637	10	BF569958	602186119	C 650	23.2	32.7	560	12	AQ141621	AQ141621	HS_3164_A
578	23.4	33.0	641	9	A1299951	qn59d02.x	C 651	23.2	32.7	565	10	BE293593	BE293593	601186770
C 579	23.4	33.0	646	9	AM950053	EST362243	C 652	23.2	32.7	569	10	B1344776	B1344776	373343.MA
C 580	23.4	33.0	649	9	A1796694	wh59g03.x	C 653	23.2	32.7	576	9	AA149637	AA149637	z139B08.s
C 581	23.4	33.0	651	10	BG387129	602455844	C 654	23.2	32.7	580	9	AV919381	AV919381	AV919381
C 582	23.4	33.0	667	10	B1331818	602982391	C 655	23.2	32.7	584	10	BG699939	BG699939	602681114
C 583	23.4	33.0	683	9	AL636704	AL636704	C 656	23.2	32.7	592	10	B1569114	B1569114	RH01302.3
C 584	23.4	33.0	684	10	BF970507	602272686	C 657	23.2	32.7	594	9	AL500732	AL500732	AL500732
C 585	23.4	33.0	690	12	CNS01RL	AL164082	C 658	23.2	32.7	600	9	A1402072	A1402072	GHO7283.3
C 586	23.4	33.0	698	9	AV710372	AV710372	C 659	23.2	32.7	614	9	A1135299	A1135299	GH12978.5
C 587	23.4	33.0	711	10	B1332966	602980089	C 660	23.2	32.7	649	10	B1821128	B1821128	603035008
C 588	23.4	33.0	729	10	B1873647	963110C06	C 661	23.2	32.7	678	12	AV920634	AV920634	AV920634
C 589	23.4	33.0	773	9	A1121713	qb99a09.x	C 662	23.2	32.7	681	9	AG140897	AG140897	Par.trog1
C 590	23.4	33.0	782	12	CNS01EB9	AL140326	C 663	23.2	32.7	686	12	AG140897	AG140897	Par.trog1
C 591	23.4	33.0	798	9	A1207840	ao68h07.x	C 664	23.2	32.7	687	9	BB615574	BB615574	BB615574
C 592	23.4	33.0	798	9	A1833019	al74c09.x	C 665	23.2	32.7	699	9	AL505164	AL505164	AL505164
C 593	23.4	33.0	810	10	B1905134	603168523	C 666	23.2	32.7	734	12	AQ689431	AQ689431	NDXB0079J
C 594	23.4	33.0	844	10	BE970772	601680128	C 667	23.2	32.7	737	9	AL523843	AL523843	AL523843
C 595	23.4	33.0	846	10	BF139734	601785386	C 668	23.2	32.7	779	12	BE412633	BE412633	MC6001.F1
C 596	23.4	33.0	851	9	AL570439	AL570439	C 669	23.2	32.7	793	12	AZ210947	AZ210947	SP_0154.B
C 597	23.4	33.0	864	10	BF795336	602260425	C 670	23.2	32.7	795	12	AG095950	AG095950	Par.trog1
C 598	23.4	33.0	871	10	B1766382	603052622	C 671	23.2	32.7	809	10	B1088888	B1088888	602854234
C 599	23.4	33.0	883	10	BG118128	602345895	C 672	23.2	32.7	816	10	B1908486	B1908486	603065249
C 600	23.4	33.0	887	10	BF689120	602185195	C 673	23.2	32.7	856	10	B1754349	B1754349	603023191
C 601	23.4	33.0	891	10	BE540883	601063002	C 674	23.2	32.7	870	10	BG402360	BG402360	602465947

C 675	23.2	32.7	879	12	CNS03CGK	AL237773 Tetraodon	C 748	23	32.4	500	10	BE495279
C 676	23.2	32.7	891	12	CNS032PC	AL225129 Tetraodon	C 749	23	32.4	502	10	BI899025
C 677	23.2	32.7	934	12	AZ546916	ENTDT177R	C 750	23	32.4	505	10	AI871114
C 678	23.2	32.7	948	10	BE249922	600942970	C 751	23	32.4	505	10	BI360371
C 679	23.2	32.7	950	10	BE900875	601673873	C 752	23	32.4	506	10	BF834074
C 680	23.2	32.7	963	9	AL542562	AL542562 AL542562	C 753	23	32.4	506	10	B016069
C 681	23.2	32.7	968	10	BE034355	BE034355 602302243	C 754	23	32.4	507	12	AQ412279
C 682	23.2	32.7	979	9	AL523849	AL523849 AL523849	C 755	23	32.4	507	10	AI741752
C 683	23.2	32.7	982	12	CNS03CPO	AL238101 Tetraodon	C 756	23	32.4	511	10	B015975
C 684	23.2	32.7	999	12	CNS03CPO	AL562722 Tetraodon	C 757	23	32.4	515	9	AI967925
C 685	23.2	32.7	1004	10	BM423806	BM423806 AGENCOURT	C 758	23	32.4	516	9	AI638781
C 686	23.2	32.7	1017	12	CNS0330M9	AL561622 Tetraodon	C 759	23	32.4	516	10	BF002145
C 687	23.2	32.7	1039	10	BE700694	BE700694 602128682	C 760	23	32.4	520	9	AM205490
C 688	23.2	32.7	1043	12	CNS02AHN	AL185864 Tetraodon	C 761	23	32.4	526	10	BI963910
C 689	23.2	32.7	1062	10	BE578023	BE578023 602091864	C 762	23	32.4	527	10	BE501473
C 690	23.2	32.7	1101	12	CNS00DEJ	AL069092 Drosophila	C 763	23	32.4	530	9	AM027982
C 691	23.2	32.7	1312	10	BE728662	BE728662 601563942	C 764	23	32.4	533	9	AI595594
C 692	23.2	32.7	1440	12	AC079960	AC079960 Pan. trogl.	C 765	23	32.4	535	10	BJ026603
C 693	23.2	32.7	1538	10	BE183050	BE183050 601809622	C 766	23	32.4	539	10	BE077914
C 694	23.2	32.7	1598	10	BE754873	BE754873 208534 MA	C 767	23	32.4	544	9	AI937105
C 695	23.2	32.7	207	10	BE874394	BE874394 IL3-ET011	C 768	23	32.4	545	10	BI430728
C 696	23.2	32.7	231	9	BM604678	BM604678 BM604678	C 769	23	32.4	547	10	BC300674
C 697	23.2	32.7	234	10	H61158	H61158 yu37f05.s1	C 770	23	32.4	562	9	AI971310
C 698	23.2	32.7	293	10	W01132	W01132 y25911.1	C 771	23	32.4	573	9	AV601137
C 699	23.2	32.7	299	9	AV543790	AV543790 AV543790	C 772	23	32.4	574	10	B015084
C 700	23.2	32.7	299	9	BB347824	BB347824 BB347824	C 773	23	32.4	583	10	BI396375
C 701	23.2	32.7	303	9	AM820835	RC2-ST030	C 774	23	32.4	584	9	AA042224
C 702	23.2	32.7	306	9	BB275536	BB275536 BB275536	C 775	23	32.4	592	10	B014497
C 703	23.2	32.7	306	10	C74759	C74759 C74759 RICE	C 776	23	32.4	593	10	B014489
C 704	23.2	32.7	326	10	C75396	C75396 C75396 Huma	C 777	23	32.4	594	10	B016953
C 705	23.2	32.7	330	9	AI910489	AI910489 w131f03.x	C 778	23	32.4	602	12	FR0004192
C 706	23.2	32.7	337	10	BF432584	BF432584 nabv4h03.x	C 779	23	32.4	615	10	B014778
C 707	23.2	32.7	339	12	AA037591	AA037591 CIT-HSP-2	C 780	23	32.4	617	10	BE903142
C 708	23.2	32.7	341	9	BB274952	BB274952 BB274952	C 781	23	32.4	622	10	BG134458
C 709	23.2	32.7	346	9	AL042304	AL042304 DREXP434M	C 782	23	32.4	625	12	AC034707
C 710	23.2	32.7	348	12	AO195361	AO195361 RPTC11-46	C 783	23	32.4	626	9	AM057581
C 711	23.2	32.7	367	9	AI082395	AI082395 ov21c03.x	C 784	23	32.4	637	10	B028656
C 712	23.2	32.7	368	10	BF874726	BF874726 IL3-ET011	C 785	23	32.4	644	10	BM425699
C 713	23.2	32.7	374	9	AJ395453	AJ395453 AJ395453	C 786	23	32.4	651	12	AC049100
C 714	23.2	32.7	390	9	AM198289	pol-D-PKO	C 787	23	32.4	655	10	BE310176
C 715	23.2	32.7	419	9	AM135599	UT-H-BIT-	C 788	23	32.4	656	10	B024608
C 716	23.2	32.7	429	9	AI768179	AI768179 w982a12.x	C 789	23	32.4	656	12	AC060182
C 717	23.2	32.7	431	9	AI394569	AI394569 t908c04.x	C 790	23	32.4	662	12	AZ986490
C 718	23.2	32.7	433	10	BF457143	BF457143 UI-M-B21-	C 791	23	32.4	663	10	B027422
C 719	23.2	32.7	436	12	AO937660	AO937660 NB6-249R	C 792	23	32.4	663	10	B027497
C 720	23.2	32.7	444	12	AO939475	AO939475 NR1-181R	C 793	23	32.4	665	10	B021044
C 721	23.2	32.7	446	12	AZ607189	AZ607189 IM0429E05	C 794	23	32.4	666	10	B017293
C 722	23.2	32.7	446	12	AO192603	AO192603 HS-2247-B	C 795	23	32.4	671	10	BI394478
C 723	23.2	32.7	449	9	AM355585	AM355585 p11c-PKO	C 796	23	32.4	674	10	B027719
C 724	23.2	32.7	450	9	AM270951	AM270951 x806f08.x	C 797	23	32.4	675	10	B021487
C 725	23.2	32.7	456	9	AI452771	AI452771 t145d01.x	C 798	23	32.4	675	10	B0207035
C 726	23.2	32.7	458	10	BE855473	BE855473 T914g01.x	C 799	23	32.4	682	10	BI256652
C 727	23.2	32.7	459	9	AM193728	AM193728 xm29h04.x	C 800	23	32.4	683	10	B021484
C 728	23.2	32.7	461	10	BI478629	BI478629 949068A03	C 801	23	32.4	685	9	AU169631
C 729	23.2	32.7	463	10	BE659920	BE659920 T9ESTzyA0	C 802	23	32.4	689	9	AL627746
C 730	23.2	32.7	465	10	BF194825	BF194825 7089a07.x	C 803	23	32.4	694	10	B0225083
C 731	23.2	32.7	466	9	AI091739	AI091739 OW59h07.x	C 804	23	32.4	696	10	BI702968
C 732	23.2	32.7	472	9	AI660973	AI660973 w120f05.x	C 805	23	32.4	715	10	BE620231
C 733	23.2	32.7	474	9	AA625678	AA625678 zu86a08.s	C 806	23	32.4	723	10	BI891816
C 734	23.2	32.7	474	10	BE374259	BE374259 601227618	C 807	23	32.4	740	10	BE563866
C 735	23.2	32.7	475	9	AI168183	AI168183 0009g06.x	C 808	23	32.4	744	10	BE576891
C 736	23.2	32.7	477	10	BE131833	BE131833 ESTa64725	C 809	23	32.4	753	10	BG432064
C 737	23.2	32.7	478	9	AI986406	AI986406 w122d07.x	C 810	23	32.4	760	10	B0679729
C 738	23.2	32.7	481	12	BE221731	BE221731 hf58e10.x	C 811	23	32.4	774	10	BF525901
C 739	23.2	32.7	481	12	BM176723	BM176723 007.M.02-	C 812	23	32.4	778	10	BE412037
C 740	23.2	32.7	481	12	CNS07FEK	AL613682 T3 and of	C 813	23	32.4	796	9	AL534550
C 741	23.2	32.7	488	10	BE528590	BE528590 602043590	C 814	23	32.4	799	10	BE778583
C 742	23.2	32.7	489	9	AL640104	AL640104 AL640104	C 815	23	32.4	822	12	BM676944
C 743	23.2	32.7	489	12	AO939489	AO939489 NR1-200R	C 816	23	32.4	826	10	BE547876
C 744	23.2	32.7	494	9	BB855311	BB855311 BB855311	C 817	23	32.4	828	10	BG242918
C 745	23.2	32.7	494	12	BM229629	BM229629 1006153D0	C 818	23	32.4	842	10	BI256797
C 746	23.2	32.7	496	10	BM141793	BM141793 if26d05.x	C 819	23	32.4	842	10	BI759025
C 747	23.2	32.7	500	10	B019346	B019346 B019346	C 820	23	32.4	845	10	BG285117
C 748	23.2	32.7	500	10	BE495279	BE495279 WHE1268_H	C 748	23	32.4	500	10	BE495279
C 749	23.2	32.7	502	10	BI899025	BI899025 480875 MA	C 749	23	32.4	502	10	BI899025
C 750	23.2	32.7	505	10	AI871114	AI871114 w179c07.x	C 750	23	32.4	505	10	AI871114
C 751	23.2	32.7	505	10	BI360371	BI360371 387249 MA	C 751	23	32.4	505	10	BI360371
C 752	23.2	32.7	506	10	BF834074	BF834074 RC3-HT023	C 752	23	32.4	506	10	BF834074
C 753	23.2	32.7	506	10	B016069	B016069 B016069	C 753	23	32.4	506	10	B016069
C 754	23.2	32.7	507	12	AQ412279	AQ412279 RPTC-11-1	C 754	23	32.4	507	12	AQ412279
C 755	23.2	32.7	507	10	AI741752	AI741752 w922e08.x	C 755	23	32.4	507	10	AI741752
C 756	23.2	32.7	511	10	B015975	B015975 B015975	C 756	23	32.4	511	10	B015975
C 757	23.2	32.7	515	9	AI967925	AI967925 wu11a02.x	C 757	23	32.4	515	9	AI967925
C 758	23.2	32.7	516	9	AI638781	AI638781 t132c04.x	C 758	23	32.4	516	9	AI638781
C 759	23.2	32.7	516	10	BF002145	BF002145 7999h08.x	C 759	23	32.4	516	10	BF002145
C 760	23.2	32.7	520	9	AM205490	AM205490 UT-H-BIT-	C 760	23	32.4	520	9	AM205490
C 761	23.2	32.7	526	10	BI963910	BI963910 l6e6e04.x	C 761	23	32.4	526	10	BI963910
C 762	23.2	32.7	527	10	BE501473	BE501473 hw32d12.x	C 762	23	32.4	527	10	BE501473
C 763	23.2	32.7	530	9	AM027982	AM027982 wv25g09.x	C 763	23	32.4	530	9	AM027982
C 764	23.2	32.7	533	9	AI595594	AI595594 AL595594	C 764	23	32.4	533	9	AI595594
C 765	23.2	32.7	535	10	BJ026603	BJ026603 BJ026603	C 765	23	32.4	535	10	BJ026603
C 766	23.2	32.7	539	10	BE077914	BE077914 228104 MA	C 766	23	32.4	539	10	BE077914
C 767	23.2	32.7	544	9	AI937105	AI937105 wp73b08.x	C 767	23	32.4	544	9	AI937105
C 768	23.2	32.7	545	10	BI430728	BI430728 949060B11	C 768	23	32.4	545	10	BI430728
C 769	23.2	32.7	547	10	BC300674	BC300674 HVSMB001	C 769	23	32.4	547</		

821	23	32.4	850	12	CNS01F1M	AL141275	Anopheles	894	22.8	32.1	634	9	BB655222
822	23	32.4	860	12	CNS03WGL	AL126396	Tetrarodon	895	22.8	32.1	642	9	AA753523
823	23	32.4	863	12	AZ194898	AL194898	SP_1029_A	896	22.8	32.1	648	10	BJ011208
824	23	32.4	893	12	CNS0349L	AL1227154	Tetrarodon	897	22.8	32.1	660	10	BJ012700
825	23	32.4	907	10	BF120447	BF120447	601756608	898	22.8	32.1	666	12	CNS040G0
826	23	32.4	930	10	BE892110	BE892110	601434617	899	22.8	32.1	672	10	BJ014750
827	23	32.4	930	10	BE903390	BE903390	601675911	900	22.8	32.1	673	10	BF578472
828	23	32.4	947	12	CNS02HMN	AL198176	Tetrarodon	901	22.8	32.1	676	10	BJ000862
829	23	32.4	948	10	BG644799	BG644799	602799225	902	22.8	32.1	679	10	BE292299
830	23	32.4	987	12	AG081063	AG081063	Par trogl	903	22.8	32.1	687	10	BJ005507
831	23	32.4	1007	10	BI757200	BI757200	603030701	904	22.8	32.1	691	10	BG338370
832	23	32.4	1031	10	BI517498	BI517498	603041775	905	22.8	32.1	707	9	AU085830
833	23	32.4	1081	10	BM479064	BM479064	AGENCOURT	906	22.8	32.1	720	10	BJ018525
834	23	32.4	1082	12	AG060354	AG060354	Par trogl	907	22.8	32.1	732	10	BE392263
835	23	32.4	1285	10	BI869094	BI869094	603395410	908	22.8	32.1	736	12	CNS03WPD
836	23	32.4	1299	10	BI695448	BI695448	603346451	909	22.8	32.1	738	10	BE300804
837	23	32.4	1313	10	BF128047	BF128047	601810715	910	22.8	32.1	749	10	BJ023096
838	23	32.4	1356	12	AG073212	AG073212	Par trogl	911	22.8	32.1	763	10	BJ019468
839	23	32.4	1426	10	BE543802	BE543802	601071641	912	22.8	32.1	774	10	BI829052
840	23	32.4	1712	10	BF182046	BF182046	601805981	913	22.8	32.1	778	10	BJ026977
841	22.8	32.1	80	12	BH216842	BH216842	100604741	914	22.8	32.1	780	10	BF237944
842	22.8	32.1	117	12	BH222812	BH222812	100610900	915	22.8	32.1	793	10	BJ025422
843	22.8	32.1	156	12	BH224161	BH224161	100611780	916	22.8	32.1	799	10	BG742367
844	22.8	32.1	190	10	R17357	R17357	Y913F07.r1	917	22.8	32.1	807	9	AL574285
845	22.8	32.1	213	9	AI431393	AI431393	0031.Catf	918	22.8	32.1	809	9	AL524403
846	22.8	32.1	222	12	BH222619	BH222619	1006108C0	919	22.8	32.1	809	10	BG744023
847	22.8	32.1	248	12	AO911695	AO911695	1MAJFV1_1	920	22.8	32.1	820	9	AL516964
848	22.8	32.1	259	12	BH229843	BH229843	1006154G0	921	22.8	32.1	832	12	CNS03GUS
849	22.8	32.1	274	10	BF963589	BF963589	PM1-NN120	922	22.8	32.1	834	10	BI858369
850	22.8	32.1	274	10	BI034672	BI034672	PM1-NN120	923	22.8	32.1	837	10	BF578222
851	22.8	32.1	295	10	BF760766	BF760766	RC4-CT068	924	22.8	32.1	855	12	CNS03071
852	22.8	32.1	295	10	BH492001	BH492001	BB492001	925	22.8	32.1	859	10	BE909478
853	22.8	32.1	329	9	AA313872	AA313872	EST185729	926	22.8	32.1	872	10	BI958014
854	22.8	32.1	329	9	BB559515	BB559515	BB559515	927	22.8	32.1	873	9	AL532848
855	22.8	32.1	334	9	AA093521	AA093521	C10075.se	928	22.8	32.1	875	9	AU122630
856	22.8	32.1	358	9	BB841162	BB841162	BB841162	929	22.8	32.1	876	10	BG827568
857	22.8	32.1	365	10	BE946866	BE946866	UI-M-BH3-	930	22.8	32.1	877	10	BF529446
858	22.8	32.1	366	9	AAW352266	AAW352266	CM2-HT013	931	22.8	32.1	877	10	BF700347
859	22.8	32.1	376	9	AAW529076	AAW529076	UI-R-BH1-	932	22.8	32.1	886	10	BI413688
860	22.8	32.1	378	10	BG658919	BG658919	TGSESTy44	933	22.8	32.1	900	9	AL537675
861	22.8	32.1	401	10	BG660899	BG660899	TGSESTy41	934	22.8	32.1	902	10	BG612175
862	22.8	32.1	402	12	BH222862	BH222862	1006109F0	935	22.8	32.1	905	10	BF796034
863	22.8	32.1	418	10	T68202	T68202	Y4C0A05.r1	936	22.8	32.1	925	12	CNS0091P
864	22.8	32.1	430	9	AAW389789	AAW389789	RC2-ST017	937	22.8	32.1	931	12	AZ208744
865	22.8	32.1	439	10	BF620054	BF620054	HVSMC001	938	22.8	32.1	940	12	CNS04J4F
866	22.8	32.1	442	9	AAW389846	AAW389846	RC2-ST017	939	22.8	32.1	946	10	BE742622
867	22.8	32.1	447	9	AAW11574	AAW11574	MT4958.mo	940	22.8	32.1	957	10	BF308474
868	22.8	32.1	464	12	AZ489690	AZ489690	1M0322114	941	22.8	32.1	969	12	AG061086
869	22.8	32.1	489	10	AA707716	AA707716	zh23d10.s	942	22.8	32.1	980	10	CNS006EN
870	22.8	32.1	497	10	BM175069	BM175069	TGSESTyB1	943	22.8	32.1	981	10	BG247009
871	22.8	32.1	497	9	AI8884846	AI8884846	w185d11.x	944	22.8	32.1	982	12	CNS03RTE
872	22.8	32.1	518	12	AZ234074	AZ234074	RPC1-23-7	945	22.8	32.1	990	10	BI155686
873	22.8	32.1	524	12	BH222724	BH222724	1006108H0	946	22.8	32.1	1007	12	CNS054AL
874	22.8	32.1	536	9	AU148139	AU148139	AU148139	947	22.8	32.1	1048	12	CNS0435B
875	22.8	32.1	540	10	BM490160	BM490160	PGP2n.pK0	948	22.8	32.1	1061	10	BM468448
876	22.8	32.1	542	10	BM175600	BM175600	TGSESTyB2	949	22.8	32.1	1073	12	AG117170
877	22.8	32.1	543	10	BJ010803	BJ010803	BJ010803	950	22.8	32.1	1097	10	BM044061
878	22.8	32.1	556	12	AO656461	AO656461	Sheared D	951	22.8	32.1	1101	12	CNS016V9
879	22.8	32.1	559	9	AA718305	AA718305	vU35g11.r	952	22.8	32.1	1116	10	BF689929
880	22.8	32.1	569	12	BJ004324	BJ004324	BJ004324	953	22.8	32.1	1120	10	BE561367
881	22.8	32.1	573	10	AZ243767	AZ243767	RPCI-23-8	954	22.8	32.1	1140	10	BM455223
882	22.8	32.1	577	12	BH224244	BH224244	1006117F0	955	22.8	32.1	1154	10	BF133099
883	22.8	32.1	582	9	AI770430	AI770430	606052E04	956	22.8	32.1	1180	10	BM455339
884	22.8	32.1	587	9	AA459583	AA459583	aa27g02.r	957	22.8	32.1	1395	12	AG083254
885	22.8	32.1	593	10	BJ002378	BJ002378	BJ002378	958	22.8	32.1	1419	10	BM471417
886	22.8	32.1	596	10	BI639464	BI639464	SD22044.5	959	22.8	32.1	1425	10	BG298750
887	22.8	32.1	597	10	BE016888	BE016888	BE016888	960	22.8	32.1	1459	10	BM470923
888	22.8	32.1	597	10	BE658460	BE658460	GM700006A	961	22.8	32.1	1508	11	AK019852
889	22.8	32.1	597	12	BH224082	BH224082	1006116G0	962	22.6	31.8	99	9	H58315
890	22.8	32.1	620	12	BH232259	BH232259	1006166G0	963	22.6	31.8	139	9	AV173532
891	22.8	32.1	624	9	AAW58372	AAW58372	EST370442	964	22.6	31.8	165	12	AO937858
892	22.8	32.1	624	10	BJ024542	BJ024542	BJ024542	965	22.6	31.8	191	10	BF476351
893	22.8	32.1	626	9	AA943098	AA943098	EST198597	966	22.6	31.8	222	9	BB451117

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967 22.6 31.8 249 9 AA602323
968 22.6 31.8 259 9 AA335076
969 22.6 31.8 266 10 AA4473
970 22.6 31.8 270 9 AA214833
971 22.6 31.8 289 9 AA065332
972 22.6 31.8 292 9 BB554752
973 22.6 31.8 313 9 A1597873
974 22.6 31.8 313 9 A1818043
975 22.6 31.8 320 9 AA401998
976 22.6 31.8 321 10 BM255295
977 22.6 31.8 323 12 BH339400
978 22.6 31.8 331 9 AJ283159
979 22.6 31.8 332 9 AV640294
980 22.6 31.8 337 9 BE119873
981 22.6 31.8 352 9 AM656299
982 22.6 31.8 352 9 AM668809
983 22.6 31.8 359 9 A1703584
984 22.6 31.8 359 12 BH468603
985 22.6 31.8 368 10 BF485114
986 22.6 31.8 369 9 AV433669
987 22.6 31.8 373 10 BF989552
988 22.6 31.8 382 9 AV628531
989 22.6 31.8 382 10 BG052442
990 22.6 31.8 384 10 N26581
991 22.6 31.8 409 9 A1923159
992 22.6 31.8 416 9 BB850493
993 22.6 31.8 416 9 AV430433
994 22.6 31.8 435 10 BF601420
995 22.6 31.8 440 10 BM483929
996 22.6 31.8 443 10 B1024741
997 22.6 31.8 446 12 A2435646
998 22.6 31.8 451 10 BG607847
999 22.6 31.8 457 9 AM315865
1000 22.6 31.8 460 10 BF202093

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ALIGNMENTS

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RESULT 1
B82759/c 520 bp DNA linear GSS 09-APR-1999
LOCUS RPlc11-17K22.TP RPlc1-11 Homo sapiens genomic clone RPlc1-11-17K22,
DEFINITION DNA sequence.
ACCESSION B82759
VERSION B82759.1
KEYWORDS GI:2869782
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE
1 (bases 1 to 520)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,F., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs: RPlc11-17K22.TVB
CONTACT Mark Adams
DEPARTMENT Department of Eukaryotic Genomics
INSTITUTE The Institute for Genomic Research
ADDRESS 9712 Medical Center Dr., Rockville, MD 20850, USA
TEL 301 838 0200
FAX 301 838 0208
EMAIL mdadams@tigr.org

```

Clones are derived from the human BAC library RPlc1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html

Seq primer: SP6
Class: BAC ends.

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FEATURES
source Location/Qualifiers

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1..520
/organism="Homo sapiens"
/db_xref="GDB:7506405"
/db_xref="taxon:9606"
/clone="RPlc1-11-17K22"
/clone_11b="RPlc1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPlc11 Human Male BAC Library"
BASE COUNT 101 a 154 c 153 g 112 t
ORIGIN

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Query Match 100.0%; Score 71; DB 12; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCAACCTGTCGACCGATCGGTCGACCGACCGACCTGGCGGAGAGACAGCTGT 60
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DB 355 GCAACCTGTCGACCGATCGGTCGACCGACCGACCGACCTGGCGGAGAGACAGCTGT 296
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QY 61 GCCCTCCGAC 71
|||||
DB 295 GCCCTCCGAC 285

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RESULT 2
BB588668 657 bp mRNA linear EST 26-OCT-2001
LOCUS BB588668
DEFINITION Musculus cDNA clone A230002D02 5', mRNA sequence.
ACCESSION BB588668
VERSION BB588668.2
KEYWORDS GI:16449788
SOURCE house mouse.
ORGANISM Mus musculus

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REFERENCE
1 (bases 1 to 657)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koude,
M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Nov 30, 2000 this sequence version replaced gi:11485212.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayata,S., Sugahara,Y., Shibata,K., Itoh,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1611-1630 (2000)
Wagl,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
Y. and Hayashizaki,Y.

```

TITLE
JOURNAL
COMMENT

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html).
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers

1..245
 /organism="Homo sapiens"
 /db_xref="GDB:7588110"
 /db_xref="taxon:9606"
 /clone="RP11-230H7"
 /clone_lib="RP11-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; RP11 Human Male BAC library"

BASE COUNT 49 a 82 c 61 g 53 t

ORIGIN

Query Match 45.1%; Score 32; DB 12; Length 245;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 TGGCGGGAGACAGCCTGTGCTCCGAC 71
 Db 245 TGGCGGGAGACAGCCTGTGCTCCGAC 214

RESULT 5
 B1552111 722 bp mRNA linear EST 05-SEP-2001
 LOCUS 603195053F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274709 5',
 DEFINITION B1552111
 mRNA sequence.

ACCESSION B1552111 GI:15439423
 VERSION B1552111
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
 Toshiyuki and Piero Carninci (RIKEN)
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM1693 row: 1 column: 14
 High quality sequence stop: 527.
 Location/Qualifiers

FEATURES

source

1..722
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 /db_xref="taxon:9606"
 /clone="IMAGE:5274709"
 /clone_lib="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI; xhoI (gtcgag
); Oligo-dT primed using primer 5'-gtttttttttttttt-3',
 size-selected for average insert size 2.5 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 151 a 197 c 228 g 146 t

ORIGIN

Query Match 41.1%; Score 29.2; DB 10; Length 722;
 Best Local Similarity 65.2%; Pred. No. 1.1e+02;
 Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 6 CTGTCCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGAGACACCTGTGCGCT 65
 Db 96 CGGTGCGTCCGCGGCGGTGGAGCGCGGAGCTAGCGAGAGAGACAGCCTGCGCCG 155

QY 66 CCGACC 71
 Db 156 CCGTCC 161

RESULT 6

AO308543/c 454 bp DNA linear GSS 22-DEC-1998
 LOCUS CITBI-EI-2525G14.TF CITBI-EI Homo sapiens genomic clone 2525G14,
 DEFINITION DNA sequence.
 ACCESSION AO308543
 VERSION AO308543.1 GI:4039505
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 454)
 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M. and
 Venter,J.C.
 Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 Unpublished (1998)
 other_GSS: CITBI-EI-2525G14.TF
 Contact: Shaying Zhao, William Nieman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@igf.org

Clones are available from Research Genetics (http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html). BAC
 end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 Location/Qualifiers

source

1..454
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 /db_xref="taxon:9606"
 /clone="2525G14"
 /clone_lib="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
 CalTech Human BAC Library D"

BASE COUNT 71 a 139 c 162 g 82 t

ORIGIN

Query Match 39.4%; Score 28; DB 12; Length 454;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 10 CCGACCCATGCGTCCGAACCGACCGACCTGGCGGAGAGACAGCCTGTGCGCTCGGA 69
 Db 368 CTGCGCCAGGTGCTAAAGCCCTCACTGCGGAGGCGGCGGAGCTGCTCGCTCGGA 309

RESULT 7
 FR0039005 605 bp DNA linear GSS 22-OCT-1999
 LOCUS

DEFINITION	Fugu rubripes GSS sequence, clone 089D07Bh9, genomic survey sequence.
ACCESSION	AL126503
VERSION	ALI26503.1 GI:6108118
KEYWORDS	GSS; genome survey sequence.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes; Tetraodontidae; Takifugu. 1 (bases 1 to 605)
AUTHORS	Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umranta,Y., Williams,G. and Brenner,S.
TITLE	Direct Submission
JOURNAL	Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelphelp.mrc.ac.uk Vector: pBluescript II KS V-type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.
FEATURES	Location/Qualifiers 1..605 /organism="Takifugu rubripes" /db_xref="taxon:31033" /clone_lib="cosmid 089D07" /clone="089D07bh9"
BASE COUNT	123 a 189 c 180 g 92 t 21 others
ORIGIN	
Query Match	38.9%; Score 27.6; DB 12; Length 605;
Best Local Similarity	72.0%; Pred. No. 3.1e+02;
Matches	36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY	4 ACCTGTCGCAGCCATGCGGTCCGACGCCAGCAGCTGGGGGAGAGAC 53 Db 89 ACCGACTGACCCGCTCCGACCGACCGACCCTGCTGGACCGAGCCGAC 138
RESULT 8	
BP305771/c	921 bp mRNA linear EST 21-NOV-2000
LOCUS	601869127F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4122991 5',
DEFINITION	mRNA sequence.
ACCESSION	BF305771
VERSION	BF305771.1 GI:11252767
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 921) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC
AUTHORS	CDNA Library Preparation: Ling Hong/Rubin Laboratory
TITLE	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
JOURNAL	DNA Sequencing by: Incyte Genomics, Inc.
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LUCM1007 row: e column: 08 High quality sequence stop: 692. Location/Qualifiers 1..921 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4122991"
DEFINITION	Fugu rubripes GSS sequence, clone 089D07Bh9, genomic survey sequence.
ACCESSION	AL126503
VERSION	ALI26503.1 GI:6108118
KEYWORDS	GSS; genome survey sequence.
SOURCE	Takifugu rubripes.
ORGANISM	Takifugu rubripes
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes; Tetraodontidae; Takifugu. 1 (bases 1 to 605)
AUTHORS	Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umranta,Y., Williams,G. and Brenner,S.
TITLE	Direct Submission
JOURNAL	Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelphelp.mrc.ac.uk Vector: pBluescript II KS V-type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.
FEATURES	Location/Qualifiers 1..605 /organism="Takifugu rubripes" /db_xref="taxon:31033" /clone_lib="cosmid 089D07" /clone="089D07bh9"
BASE COUNT	123 a 189 c 180 g 92 t 21 others
ORIGIN	
Query Match	38.9%; Score 27.6; DB 12; Length 605;
Best Local Similarity	72.0%; Pred. No. 3.1e+02;
Matches	36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY	4 ACCTGTCGCAGCCATGCGGTCCGACGCCAGCAGCTGGGGGAGAGAC 53 Db 89 ACCGACTGACCCGCTCCGACCGACCGACCCTGCTGGACCGAGCCGAC 138
RESULT 8	
BP305771/c	921 bp mRNA linear EST 21-NOV-2000
LOCUS	601869127F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4122991 5',
DEFINITION	mRNA sequence.
ACCESSION	BF305771
VERSION	BF305771.1 GI:11252767
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 848) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC
AUTHORS	CDNA Library Preparation: CLONETECH Laboratories, Inc.
TITLE	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
JOURNAL	DNA Sequencing by: Incyte Genomics, Inc.
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM1649 row: f column: 22 High quality sequence stop: 550. Location/Qualifiers 1..848 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4775061" /clone_lib="NIH_MGC_61" /tissue_type="embryonal carcinoma" /lab_host="DH10B (TI phage-resistant)" /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1; SfiI (ggcgccctggccc); Site:2; SfiI (ggccatcatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCTC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC

BASE COUNT 214 a 234 c 242 g 158 t
ORIGIN

Query Match 38.0%; Score 27; DB 10; Length 848;
Best Local Similarity 62.7%; Pred. No. 4.8e+02;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 CAACGTCTCCGACCATGCGGTCCGAAACCGCAGCACTGCGGCGAGAGACAGCCGTGTG 61
DB 655 CCACGGGGCGCCGACACAGCGGGCCCGGACTGCGAGGACCTATGCAAGCAAACTGCAGAGAG 714

QY 62 CCCTCCG 68
DB 715 CCTACCG 721

RESULT 10
LOCUS BF527152 673 bp mRNA EST 11-DEC-2000
DEFINITION 60203982F2 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4177685
ACCESSION BF527152
VERSION BF527152.1 GI:11614515
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 673)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9484 row: 1 column: 06
High quality sequence stop: 143.
Location/Qualifiers
1. 673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="NCI_CGAP_Brn67"
/clone_2ib="IMAGE:4177685"
/issue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPOK6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 105 a 167 c 273 g 128 t
ORIGIN

Query Match 37.5%; Score 26.6; DB 10; Length 673;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 TGTCCGACCATGCGGTCCGAAACCGCAGCACTGCGGCGAGAGACAGCCGTGTGCC 63
DB 48 TCTCCACCCAGCGCTCTGTGTCGGGTGAGCGGAGGACCGGCTGTGGC 104

RESULT 11
LOCUS BF541519 799 bp mRNA EST 11-DEC-2000
DEFINITION 602067882F1 NIH_MGC_58 Homo sapiens CDNA clone IMAGE:4066892 5',

ACCESSION mRNA sequence.
VERSION BF541519
LOCUS BF541519.1 GI:11628900
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM905 row: c column: 21
High quality sequence stop: 524.
Location/Qualifiers
1. 799
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:4066892"
/clone_2ib="NIH_MGC_58"
/issue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggccatctagcc);
Double-stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACATG-dt(30)BN-3'
sequence: (where B = A, C, G or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 270 a 161 c 161 g 207 t
ORIGIN

Query Match 37.5%; Score 26.6; DB 10; Length 799;
Best Local Similarity 63.1%; Pred. No. 6.1e+02;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 4 ACCTGTCCGACCATGCGGTCCGAAACCGCAGCACTGCGGCGAGAGACAGCCGTGTGCC 63
DB 773 ACCGGCCGAAACCTGCGGTTCGAACCCGCCCGCTTTTGGGAGACGCCCTGTGCT 714

QY 64 CTCCG 68
DB 713 GCCCG 709

RESULT 12
LOCUS BF382133 894 bp mRNA EST 27-NOV-2000
DEFINITION 601814891F2 NIH_MGC_56 Homo sapiens CDNA clone IMAGE:4048894 5',
ACCESSION BF382133
VERSION BF382133
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LICM880 row: e column: 23
High quality sequence stop: 425.
Location/Qualifiers
1. .894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4048894"
/clone_lib="NIH_MGC_56"
/issue_type="Primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (99cgcgcgcgc); Site_2: SfiI (99ccatcgcgc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 249 a 234 c 238 g 173 t
ORIGIN

Query Match 37.5%; Score 26.6; DB 10; Length 894;
Best Local Similarity 63.1%; Pred. No. 6.2e+02;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2 CAACGTGCGACCCATCGCTCCGACCGACCGACTGGCGGAGACAGACGCTGTG 61
DB 206 CAGGCTGCCACACATTCCTGCTCGCTCAGCCTCCGAGTACCTGGACTGTCAGTG 147
QY 62 CCCTC 66
DB 146 CCCCC 142

RESULT 13
CNS02R80/c 909 bp DNA linear GSS 14-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
DEFINITION 159B11 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL210273.1 GI:7869092
VERSION AL210273
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthomorpha; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 909)
Roeest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 909)
Roeest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using
JOURNAL Tetraodon nigroviridis DNA sequence
REFERENCE Unpublished
AUTHORS 3 (bases 1 to 909)
TITLE Genoscope.
JOURNAL Direct Submission
COMMENT Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.
Location/Qualifiers
1. .909
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_image="159B11"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG159CA06SP1-end : PUC-ori"

BASE COUNT 170 a 256 c 287 g 171 t 25 others
ORIGIN

Query Match 37.5%; Score 26.6; DB 12; Length 909;
Best Local Similarity 60.9%; Pred. No. 6.2e+02;
Matches 42; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY 3 AACCTGTCCGACCCATCGCTCCGACCGACCGACTGGCGGAGACAGACGCTGTG 62
DB 380 AACGCTTCCACCGACGAGCGGTCGCCGACCTGAGAGAGACGCCCTCG 321
QY 63 CCTCGACC 71
DB 320 CCGCGGCC 312

RESULT 14
BG697293/c 937 bp RNA linear EST 07-MAY-2001
LOCUS BG697293
DEFINITION mRNA sequence.
ACCESSION BG697293
VERSION BG697293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 937)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LRAM10699 row: f column: 11
High quality sequence stop: 857.
Location/Qualifiers
1. .937
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4803466"
/clone_lib="NCI CGAP SKN3"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT	165 a	276 c	326 g	170 t
ORIGIN				
Query Match	37.5%; Score 26.6; DB 10; Length 937;			
Best Local Similarity	63.1%; Pred. No. 6.3e+02;			
Matches	41; Conservative	0; Mismatches	24; Indels	0; Gaps
QY	63	CCTCC 67		
Db	55	CCGCC 51		
RESULT 15				
LOCUS	BF583863	416 bp	mRNA	linear
DEFINITION	602096861P1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4216815 5'			
ACCESSION	BF583863			
VERSION	BF583863.1 GI:11657581			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 416)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM9794 row: j column: 16 High quality sequence stop: 336. Location/Qualifiers 1. 416 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4216815" /clone_lib="NCI_CGAP_CO24" /lab_host="DH10B (TI phage-resistant)" /note="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." BASE COUNT 65 a 147 c 112 g 92 t ORIGIN			
Query Match	36.9%; Score 26.2; DB 10; Length 416;			
Best Local Similarity	63.5%; Pred. No. 7.4e+02;			
Matches	40; Conservative	0; Mismatches	23; Indels	0; Gaps
QY	1	GCACCTCTCGACCCATGCGGTCCGAACCGACGACCTGGCGGAGAGACAGCCTGT	60	
Db	50	GAAATCATGACAGGCCCATCTTCGCTACCGACACTACTGTGATGGCTGGAACAGCCCTT	109	
QY	61	GCC 63		
Db	110	CCC 112		
RESULT 16				
LOCUS	AL515844/c			

LOCUS	AL551844	811 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL551844 LTR1.NFL006.PL2 Homo sapiens CDNA clone CS0D1061YD17 5				
ACCESSION	AL551844				
VERSION	AL551844.1	GI:12890181			
KEYWORDS	EST.				
ORGANISM	Homo sapiens				
SOURCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 811)				
AUTHORS	Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Location/Qualifiers				
SOURCE	1. 811				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="CS0D1061YD17"				
	/clone_id="LTR1.NFL006.PL2"				
	/issue_type="Placenta"				
	/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand CDNA was primed with a NotI-01910(dT) primer. Five prime end enriched, double-stranded and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. contact : Peng Liang life technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liliang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	125 a	215 c	249 g	167 t	55 others
ORIGIN					
Query Match	36.9% Score 26.2; DB 9; Length 811;				
Best Local Similarity	58.0%; Prem. No. 8e+02;				
Matches 40; Conservative	3; Mismatches 26; Indels 0; Gaps 0;				
QY	3 AACGTCGCGACCATGTCGGTCCGACGACCGACCGCGGGGAGAGACAGCCTGTCG 62				
DB	462 MACCTGTAAGCCCTCCCTCCCTCGGCGACGCTCAGAGCCAGCAGAGCCCTCTGTGG 403				
QY	63 CCTCGACC 71				
DB	402 CCTCGGRC 394				
RESULT 17					
LOCUS	AM427436	200 bp	mRNA	linear	EST 25-APR-2001
DEFINITION	61386 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.				
ACCESSION	AM427436				
VERSION	AM427436.1	GI:6953383			
KEYWORDS	EST.				
SOURCE	cow.				
ORGANISM	Bos taurus				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 200)				
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pette,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				

Best Local Similarity 62.1%; Pred. No. 9e+02;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 6 CTTCCGACCGATCGGTCGACACCGACCGCTGGCGGGAGAGACACCGTGGCTT 65
Db 78 CTACCGACCGACCGACCGCGCGCGCTGCTCCCGCTGAGCGCCGCGCGCGCC 137

QY 66 CCGACC 71
Db 138 CCGATC 143

RESULT 20
BF167284 779 bp mRNA linear EST 30-OCT-2000
LOCUS 601775758F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017351 5',
DEFINITION mRNA sequence.
ACCESSION BF167284
VERSION BF167284.1 GI:11047636
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 779)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9266 row: c column: 16
High quality sequence start: 7
High quality sequence stop: 627.
Location/Qualifiers
1..779
/organism="Mus musculus"
/strain="C57BL/6J (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:4017351"
/tissue_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 197 a 225 c 220 g 137 t

ORIGIN
Query Match 36.6%; Score 26; DB 10; Length 779;
Best Local Similarity 65.5%; Pred. No. 9e+02;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 12 GACCCATCGGTCGACACCGACCGCTGGCGGGAGAGACACCGTGGCTT 69
Db 93 GAACCCAGAGCGCGGACCTGACCGACCGCTGAGCGACCTGAGCCACCA 150

RESULT 21
N30773 555 bp mRNA linear EST 05-JAN-1996
LOCUS YW74907.s1 Soares,placenta,8to9weeks,2Nbp8to9w Homo sapiens cDNA
DEFINITION clone IMAGE:258012.3' similar to gb: X07868.mal PUTATIVE
INSULIN-LIKE GROWTH FACTOR II ASSOCIATED (HUMAN);, mRNA sequence.
ACCESSION N30773

VERSION N30773.1 GI:1149293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 555)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marris,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviskis,E., Waterston
R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 388
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 388.
Location/Qualifiers
1..555
/organism="Homo sapiens"
/db_xref="GDB:3887622"
/db_xref="taxon:9606"
/clone="IMAGE:258012"
/tissue_lib="Soares,placenta,8to9weeks,2Nbp8to9w"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pRTT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTACCATCTGAGTGGAGCGGCGGAGATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Felima Bonaldo."

BASE COUNT 100 a 154 c 177 g 121 t 3 others

ORIGIN
Query Match 36.3%; Score 25.8; DB 10; Length 555;
Best Local Similarity 60.9%; Pred. No. 9.9e+02;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 3 AACCTGTCGACCGATCGGTCGACACCGACCGCTGGCGGGAGAGACACCGTGGC 62
Db 432 AACCTGTCGACCGCTTCCCTCGGCGACGCTGAGCGACCGACCGCCCTCTGTGG 373

QY 63 CTTCCGACC 71
Db 372 CTTCCGAGC 364

RESULT 22
AJ395984 631 bp mRNA linear EST 25-JAN-2001
LOCUS AJ395984 dfa2426 Gallus gallus cDNA clone 24n20r1, mRNA sequence.
ACCESSION AJ395984
VERSION AJ395984.1 GI:7127460
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus;
Phasianinae; Gallus.
1 (bases 1 to 631)

		/lab host="E. coli EMDH10B"	
		/note="vector: pcmsport6; Library made from equivalent	
		pools of total RNA isolated from each tissue at different	
		ages. Single pass sequencing from 5'-end"	
BASE COUNT		106 a	229 c 196 g 116 t
ORIGIN			
QY	Query Match	36.3%	Score 25.8; DB 10; Length 647;
	Best Local Similarity	63.9%	Pred. No. 1e+03;
	Matches 39; Conservative	0; Mismatches 22; Indels 0; Gaps 0;	
Db	1	GCACCTGCTCCGACCCATCGGTCGGAACCGCAGCAGCTGTGGCGGAGAGACAGCCTGT	60
	215	GCCACATACCAACCTCGCGGGGCTGAGCCTTCACACGCCCGGCGAGAGACAGCCTTCT	274
QY	61 G 61		
	275 G 275		
RESULT 24			
LOCUS	BF527152/c	673 bp	mRNA linear EST 11-DEC-2000
DEFINITION	602039822F2 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177685		
ACCESSION	BF527152		
VERSION	BF527152.1	GI:11614515	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 673)		
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@mail.nih.gov		
	Tissue Procurement: David N. Louis, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLM9484 row: 1 column: 06		
	High quality sequence stop: 143.		
FEATURES			
Source			
1..673			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="IMAGE:4177685"			
/clone_lib="NCI CGAP_Brn67"			
/tissue_type="anaplastic oligodendroglioma with 1p/19q			
loss"			
/lab_host="DH10B (T1 phage-resistant)"			
/note="Organ: brain; Vector: PCMV-SpORT6; site_1: NotI;			
site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.			
Average insert size 2.3 kb. Constructed by Life			
Technologies. Note: this is a NCI-CGAP Library."			
BASE COUNT	105 a	167 c	273 g 128 t
ORIGIN			
Query Match	36.3%	Score 25.8; DB 10; Length 673;	
Best Local Similarity	63.9%	Pred. No. 1e+03;	
Matches 39; Conservative	0; Mismatches 22; Indels 0; Gaps 0;		
QY	1	GCACCTGCTCCGACCCATCGGTCGGAACCGCAGCAGCTGTGGCGGAGAGACAGCCTGT	60
	115	GCACAGCATCGCCAGCACCGGTCCCTCCCGCTAGCCCTGACCGGACAGAGACAGCCTTG	56
Db	61 G 61		
	275 G 275		
QY	1		

Db	55	G	55
RESULT 25	A1373475	136 bp	mRNA
LOCUS	qz46b05.x1 NCI-CGAP_Kid11 Homo sapiens	cdna clone	IMAGE:2029905 3'
DEFINITION	mRNA sequence.		
VERSION	A1373475.1	GI:4153341	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 136)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapb-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bhrp/image/image.html Seq primer: -40UP from Gbpco.		
FEATURES	Location/Qualifiers		
SOURCE	1..136 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2029905" /clone_lib="NCI CGAP_Kid11" /lab_host="DH10B" /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAPR purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	24 a 42 c 41 g 29 t		
ORIGIN			
Query Match	36.1%, Score 25.6; DB 9; Length 136;		
Best Local Similarity	66.1%; Pred. No. 9.5e+02;		
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;			
Db	48 GCACACTGCCCTCCCGAGGTGGGTGAAGCCAGCAGGAGGAGGACAGATGC	103	
Y	1 GCACCTGTCGACCCATGCGTCCGAGCCGACCGACGACTGGCGGAGAGACAC	56	
LOCUS	BF476113		
DEFINITION	BF476113 136 bp mRNA		
ACCESSION	h177f04.x1 NCI-CGAP_Kid11 Homo sapiens		
VERSION	BF476113		
KEYWORDS	BF476113.1 GI:11546940		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
DEFINITION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 136)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapb-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bhrp/image/image.html Seq primer: -40UP from Gbpco.		
FEATURES	Location/Qualifiers		
SOURCE	1..136 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2029905" /clone_lib="NCI CGAP_Kid11" /lab_host="DH10B" /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAPR purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	24 a 42 c 41 g 29 t		
ORIGIN			
Query Match	36.1%, Score 25.6; DB 9; Length 136;		
Best Local Similarity	66.1%; Pred. No. 9.5e+02;		
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;			
Db	48 GCACACTGCCCTCCCGAGGTGGGTGAAGCCAGCAGGAGGAGGACAGATGC	103	
Y	1 GCACCTGTCGACCCATGCGTCCGAGCCGACCGACGACTGGCGGAGAGACAC	56	
LOCUS	BF476113		
DEFINITION	BF476113 136 bp mRNA		
ACCESSION	h177f04.x1 NCI-CGAP_Kid11 Homo sapiens		
VERSION	BF476113		
KEYWORDS	BF476113.1 GI:11546940		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
DEFINITION	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 136)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapb-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/bhrp/image/image.html Seq primer: -40UP from Gbpco.		
FEATURES	Location/Qualifiers		
SOURCE	1..136 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2029905" /clone_lib="NCI CGAP_Kid11" /lab_host="DH10B" /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAPR purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	24 a 42 c 41 g 29 t		
ORIGIN			
Query Match	36.1%, Score 25.6; DB 9; Length 136;		
Best Local Similarity	66.1%; Pred. No. 9.5e+02;		
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;			

AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .					
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
JOURNAL	Unpublished (1997)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bs-riemail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.					
	CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Data distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN, send email to: info@image.lnl.gov from Glbcop.					
FEATURES	Seq primer: -40UP from Glbcop.					
source	Location/Qualifiers 1..136 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:313452" /clone_lib="NCI_CGAP_Kid11" /lab_host="DH10B" /note="Organ: kidney; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP preparation, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAS from a pool of 5,000 clones made from the same library (cloneids 13223376-13233911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."					
BASE COUNT	24 a 42 c 41 g 29 t					
ORIGIN						
Query Match	36.1%; Score 25.6; DB 10; Length 136;					
Best Local Similarity	66.1%; Pred. No. 9.5e+02;					
Matches	37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;					
1 GCACCTGTCCGACCATGCAGTCGGACGCCGACCTGCGCGAGACAGCAGC	56					
Db 48 GCACACTGCCCTCCAGTGAGGTGAGGACCCAGCGACGAGGAGAGAGATGC	103					
RESULT 27						
LOCUS	AW513012 142 bp mRNA linear EST 03-MAR-2000					
DEFINITION	x176d06.x1 NCI_CGAP_Utl Homo sapiens CDNA clone IMAGE:2792386 3', mRNA sequence.					
ACCESSION	AW513012					
VERSION	AW513012.1 GI:7151090					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 142) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
AUTHORS	Unpublished (1997)					
TITLE	Contact: Robert Strausberg, Ph.D. Email: cga@bs-riemail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.					
JOURNAL	CDNA Library Preparation: Life Technologies, Inc.					
COMMENT	CDNA Sequencing by: Greg Lennon, Ph.D. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov/image/html/lresources.shtml Seq primer: -40UP from Glbcop.					
FEATURES	Location/Qualifiers					

```
source
1. 142
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2792386"
/clone_lib="NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

BASE COUNT      26 a      42 c      42 g      32 t
ORIGIN

Query Match      36.1%; Score 25.6; DB 9; Length 142;
Best Local Similarity 66.1%; Pred. No. 9.6e+02;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY      1 GCACCTGTCCGACCATGCGGTCCGACCGCAGCAGTGGCGGAGACAGC 56
Db      51 GCACACTGCCCTTCCACAGGTGGGTGAAGCCCGACGAGGAGCAGATGC 106

RESULT 28
AM169520      144 bp      mRNA      linear      EST 12-NOV-1999
LOCUS      xj29e01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2658648 3,
DEFINITION      mRNA sequence.
ACCESSION      AM169520
VERSION      AM169520.1 GI:6401128
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 144)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
CONTACT      Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

FEATURES
source
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 144
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2658648"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"

BASE COUNT      27 a      42 c      41 g      34 t
ORIGIN

Query Match      36.1%; Score 25.6; DB 9; Length 144;
Best Local Similarity 66.1%; Pred. No. 9.6e+02;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
```

```
OY      1 GCACCTGTCCGACCATGCGGTCCGAAACCGACGACCTGGCGGAGACAGC 56
Db      53 GCACACTGCCCTTCCACAGGTGGGTGAAGCCCGACGAGGAGCAGATGC 108

RESULT 29
A1183699      258 bp      mRNA      linear      EST 29-OCT-1998
LOCUS      gel5c07.x1 Soares_fetal_lung_NBH119W Homo sapiens cDNA clone
DEFINITION      IMAGE:1739052 3', mRNA sequence.
ACCESSION      A1183699
VERSION      A1183699.1 GI:3734337
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 258)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
CONTACT      Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 684 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 225.
Location/Qualifiers
1. 258
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1739052"
/clone_lib="Soares_fetal_lung_NBH119W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGTGGAGGAGCGCCCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBH119W."

BASE COUNT      49 a      79 c      82 g      48 t
ORIGIN

Query Match      36.1%; Score 25.6; DB 9; Length 258;
Best Local Similarity 66.1%; Pred. No. 1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY      1 GCACCTGTCCGACCATGCGGTCCGACCGCAGCAGTGGCGGAGACAGC 56
Db      58 GCACACTGCCCTTCCACAGGTGGGTGAAGCCCGACGAGGAGCAGATGC 113

RESULT 30
A1383281      275 bp      mRNA      linear      EST 18-MAR-1999
LOCUS      tc77d04.x1 Soares_NhMPU_S1 Homo sapiens cDNA clone IMAGE:2070631
DEFINITION      3', mRNA sequence.
ACCESSION      A1383281
VERSION      A1383281.1 GI:4196062
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE 1 (bases 1 to 275)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 392 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 274.
Location/Qualifiers
1. 275
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2070631"
/clone_lib="Soares-NHMP_LSI"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below): Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NbHPV, and fetal heart NbH19M) were mixed, and 58 circles
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 58 a 84 c 94 g 39 t
ORIGIN
Query Match 36.1%; Score 25.6; DB 9; Length 275;
Best Local Similarity 66.1%; Pred. No. 1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy 1 GCAACCTGCGACCCATGCGTCCGACCGACCGACCTGGCGGAGACAGC 56
Db 39 GCACACTGCCCTTCCAGGTGGGTGAAGCCGACCGACGAGGAGGATGC 94
RESULT 31 282 bp mRNA linear EST 02-DEC-1998
LOCUS AT1270131
DEFINITION q163906.x1 NCI-CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959994 3',
mRNA sequence.
ACCESSION AT1270131
VERSION AT1270131.1 GI:3889298
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 282)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Insert Length: 1470 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 227.
Location/Qualifiers
1. 282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1959994"
/clone_lib="NCI-CGAP_Eso2"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site_1: SalI
; Site_2: NotI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.1 kb. Life Technologies catalog
#: 11502-010"
BASE COUNT 59 a 86 c 93 g 44 t
ORIGIN
Query Match 36.1%; Score 25.6; DB 9; Length 282;
Best Local Similarity 66.1%; Pred. No. 1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy 1 GCAACCTGCGACCCATGCGTCCGACCGACCGACCTGGCGGAGACAGC 56
Db 47 GCACACTGCCCTTCCAGGTGGGTGAAGCCGACCGACGAGGAGGATGC 102
RESULT 32 295 bp mRNA linear EST 29-NOV-1998
LOCUS AT1206415
DEFINITION q922908.x1 NCI-CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761854 3',
mRNA sequence.
ACCESSION AT1206415
VERSION AT1206415.1 GI:3765087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 295)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Insert Length: 379 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 295
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1761854"
/clone_lib="NCI-CGAP_Kid3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3D vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldi."

JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 512 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 286.
Location/Qualifiers
1.301
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2312266"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 63 a 89 c 98 g 51 t
ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 301;
Best Local Similarity 66.1%; Pred. No. 1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACCTGCCAGCCATGCCGTCCGACCGACCGACTGGCGGAGAGACAGC 56
DB 50 GCACACTGCCCTCCAGGTGGGTGAACCCAGCAGCAGGAGAGATGTC 105

RESULT 36
AM514612 330 bp mRNA linear EST 03-MAR-2000
LOCUS xus6911.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2808644 3',
DEFINITION mRNA sequence.
ACCESSION AM514612
KEYWORDS AM514612.1 GI:7152694
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 330)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/lresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 319.

JOURNAL
COMMENT

FEATURES
Source Location/Qualifiers
1.330
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2808644"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

BASE COUNT 70 a 97 c 104 g 58 t 1 others
ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 330;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACCTGCCAGCCATGCCGTCCGACCGACCGACTGGCGGAGAGACAGC 56
DB 57 GCACACTGCCCTCCAGGTGGGTGAACCCAGCAGCAGGAGAGATGTC 112

RESULT 37
A1358269 333 bp mRNA linear EST 15-FEB-1999
LOCUS qw19907.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991580 3',
DEFINITION mRNA sequence.
ACCESSION A1358269
KEYWORDS A1358269.1 GI:4109890
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 333)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 2174 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 286.
Location/Qualifiers
1.333
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1991580"
/clone_lib="NCI_CGAP_Ut3"
/tissue_type="poorly differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

BASE COUNT 67 a 98 c 110 g 58 t
ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 333;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACACTGTCGCCACCATGGGTCGCCAGCCGACCGACCTGGCGGAGACAGC 56
111 111 11 1111 11 111 111111 111 1111 11

Db 56 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGATGC 111

RESULT 38
AI268186 342 bp mRNA linear EST 29-JAN-1999
LOCUS q199h05.x1 Soares_NhMHPu_S1 Homo sapiens cDNA clone IMAGE:1880505
DEFINITION 3', mRNA sequence.
ACCESSION AI268186
VERSION AI268186.1 GI:3887353
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 342)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 607 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 301.

FEATURES
source
1.342
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1880505"
/clone_lib="Soares_NhMHPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDM, pregnant uterus
NBHPU, and fetal heart NBH11W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 72 a 108 c 116 g 46 t

ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 342;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACACTGTCGCCACCATGGGTCGCCAGCCGACCGACCTGGCGGAGACAGC 56
111 111 11 1111 11 111 111111 111 1111 11
Db 39 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGATGC 94

RESULT 39
AI718905 385 bp mRNA linear EST 10-JUN-1999
LOCUS as26f09.x1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
DEFINITION IMAGE:2334665 3', mRNA sequence.
ACCESSION AI718905
VERSION AI718905.1 GI:5036161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 385)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R., and Wilson, R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 347.

FEATURES
source
1.385
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2334665"
/clone_lib="Bartshead colon HPLRB7"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCGATTCGATCGAAGTGGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' ATTCTACTAGTAT 3' and 5' ATTCTAGTC 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Bartshead."

BASE COUNT 77 a 130 c 123 g 55 t

ORIGIN

Query Match 36.1%; Score 25.6; DB 9; Length 385;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACACTGTCGCCACCATGGGTCGCCAGCCGACCGACCTGGCGGAGACAGC 56
111 111 11 1111 11 111 111111 111 1111 11
Db 42 GCACACTGCCCTTCCAGGTGGGTGAAGCCAGCAGGAGGAGATGC 97

RESULT 40
AI336989 386 bp mRNA linear EST 15-FEB-1999
LOCUS qx82d12.x1 NCI-CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009015 3',
DEFINITION mRNA sequence.
ACCESSION AI336989
VERSION AI336989.1 GI:4073916
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 386)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.

[illegible]

BASE COUNT	82 a	146 c	142 g	72 t	
Query Match	36.1%	Score 25.6;	DB 10;	Length 442;	
Best Local Similarity	66.1%;	Pred. No. 1.1e+03;			
Matches	37;	Conservative	0;	Mismatches 19;	Indels 0;
				Gaps	0;
Db	45	GCACACTGCCCCCTCCAGCTGGGTGAAGCCGACGACGAGGAGGAGAGCATGC	100		
RESULT 49	1	GCACCTGTCCGACCCATGCGTCCGAGACCGACGACCTGGCGGGAGACAGAC	56		
LOCUS	W02503	444 bp	mRNA	linear	EST 18-APR-1996
DEFINITION	zc64g01.s1 Soares_fetal_heart_NbH19W	Homo sapiens	cDNA clone		
ACCESSION	W02503	IMAGE:327120	3', mRNA sequence.		
VERSION	W02503.1	GI:1274694			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucab,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE	The Mashu-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET				
FEATURES	High quality sequence stop: 280.				
Source	Location/Qualifiers				
	1..444				
	/organism="Homo sapiens"				
	/db_xref="GDB:1261322"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:327120"				
	/clone_lib="Soares_fetal_heart_NbH19W"				
	/sex="unknown"				
	/dev_stage="19 weeks"				
	/lab_host="DH10B (ampicillin resistant)"				
	/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site:1 Not I; Site:2 Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAATGAGTGAGCGCGCCGACATCTTTTCTTTTCTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a C _{ot} = 5. Library constructed by M.Felima Bernaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19W."				
BASE COUNT	84 a	140 c	143 g	75 t	2 others
ORIGIN					
Query Match	36.1%	Score 25.6;	DB 10;	Length 444;	
Best Local Similarity	66.1%;	Pred. No. 1.1e+03;			
Matches	37;	Conservative	0;	Mismatches 19;	Indels 0;
				Gaps	0;
	1	GCACCTGTCCGACCCATGCGTCCGAGACCGACGACCTGGCGGGAGACAGAC	56		

Db 39 GCACACTGCCCTTCCAGGTGGGTGAAGCCGACGACGAGGAGGAGATGC 94

RESULT 50

LOCUS AI978690

DEFINITION AI978690 457 bp mRNA linear EST 08-MAR-2000
w758c12.x1 NCI_CGAP-Ut1 Homo sapiens cDNA clone IMAGE:2491894 3',
mRNA sequence.

ACCESSION AI978690

VERSION AI978690.1 GI:5803720

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 457)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bdrrp/image/image.html

Insert Length: 1599 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 352.

Location/Qualifiers

1. 457

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2491894"

/clone_id="NCI_CGAP-Ut1"

/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Life Technologies catalog #:

11538-014"

BASE COUNT 88 a 150 c 150 g 68 t 1 others

ORIGIN

Query Match

36.1%; Score 25.6; DB 9; Length 457;

Best Local Similarity 66.1%; Pred. No. 1.1e+03;

Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GCACACTGTCGACCCATCGCGTCCGAAACCCGACCGACCTGGGGGGGAGAGACAGC 56

Db 30 GCACACTGTCCTTCCAGGGGGGGGAGAGCCGACGACGAGGAGGAGATGC 85

Search completed: November 1, 2002, 17:28:53
Job time : 1851 secs